

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:03:25 ; Search time 61.7538 Seconds
(without alignments)
352.133 Million cell updates/sec

Title: US-09-114-285A-31

Perfect score: 718

Sequence: 1 MRVLILLWLFAPFGLISDV.....LARTAMDYQGQTSVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	718	100.0	137	13 AAR28671	ppm-h1 protein pro
2	593.5	82.7	134	24 ABB82796	Antibody 806 varia
3	588	81.9	136	21 AAB15672	Murine 5B3 antibod
4	562.5	78.3	136	17 AA011144	Mab 1.4 heavy chai
5	562.5	78.3	136	19 AA044169	Monoclonal antibod
6	538	74.9	138	13 AAR29012	pUC-RVh-PM1f. Syn
7	538	74.9	138	13 AAR29014	pUC-RVh-PM1f-4. S
8	537	74.8	260	21 AAY55075	Single chain Fv pr
9	537	74.8	367	21 AAY55078	Single chain Fv pr

10	537	74.8	381	21	AAY55079	Single chain Fv pr
11	537	74.8	519	21	AAY55080	Single chain Fv pr
12	537	74.8	546	21	AAY55074	Single chain Fv pr
13	537	74.8	626	21	AAY55081	Single chain Fv pr
14	537	74.8	640	21	AAY55082	Single chain Fv pr
15	534	74.4	119	18	AA001584	Lead binding MAb 1
16	534	74.4	130	21	AA085196	Heavy chain amino
17	526	73.3	130	14	AAR33308	MAE13 heavy chain.
18	518.5	72.2	240	14	AAR34510	Fv(TU27). Homo sa
19	517	72.0	256	21	AAY55072	Interleukin-6 spec
20	514	71.6	119	24	AB989805	Variable region an
21	514	71.6	119	24	AB989806	Variable region an
22	512.5	71.4	140	18	AA021937	Variable heavy sub
23	512.5	71.4	140	20	AAY05267	Antibody 24-31 hum
24	512.5	71.4	140	23	ABG98318	Murine wild-type a
25	510	71.0	126	13	AAR24722	Sequence encoded b
26	505.5	70.4	225	15	AAB63118	Heavy chain of 58.
27	501	69.8	119	24	AB989808	Variable region an
28	500.5	69.7	114	15	AAR48617	Sequence of the mo
29	499.5	69.6	118	24	ABP58448	Humanised antibody
30	499.5	69.6	331	21	AAY95781	5H7 single chain a
31	499	69.5	213	16	AAR64201	Monoclonal antibod
32	497.5	69.3	136	21	AAY94391	Mouse VH group I(A
33	496	69.1	118	17	AA000829	Variable heavy cha
34	496	69.1	118	18	AA019015	Anti-human FasL an
35	495.5	69.0	121	21	AAY95776	Antibody 5H7 heavy
36	495.5	69.0	122	13	AAR24721	Sequence of a chim
37	493	68.7	117	19	AA039809	Variable domain of
38	491.5	68.5	117	11	AA070318	VH domain of antib
39	491.5	68.5	117	17	AA014486	Monoclonal antibod
40	491.5	68.5	117	17	AAR99875	Monoclonal antibod
41	478.5	66.6	241	22	AAB36827	G28.5 sfv protein.
42	478.5	66.6	496	22	AAB36828	BD1-G28.5 fusion g
43	476.5	66.4	118	24	ABP58447	Humanised antibody
44	476.5	66.4	140	18	AA021935	Variable heavy sub
45	476.5	66.4	140	20	AAY05265	Antibody 24-31 hum

ALIGNMENTS

RESULT 1
AAR28671
ID AAR28671 standard; Protein; 137 AA.

AC AAR28671;
AC AAR28671;
DT 25-MAR-2003 (updated)
DT 30-MAR-1993 (first entry)
XX XX
DE ppm-hi protein product.
XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
KW plasmid; ppm-k3; ppm-h1.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..18 /note= "Signal peptide"
FT Protein 19..137 /note= "Mature peptide"

XX WO9219759-A1.
XX PN
XX 12-NOV-1992.
XX PD
XX Mab 1.4 heavy chai
XX PF
XX 24-APR-1992; 92WO-JP00544.
XX PR
XX 25-APR-1991; 91JP-0095476.
XX PR 19-FEB-1992; 92JP-0032084.
XX

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PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX
DR WPI; 1992-398882/48.
DR N-PSDB; AAQ30756.
XX
XX Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
XX
PS Disclosure; Page 122-123; 207pp; Japanese.
XX
XX The sequences given in AAR28670-71 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognizes human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 137 AA;
Query Match 100.0%; Score 718; DB 13; Length 137;
Best Local Similarity 100.0%; Pred. No. 8.7e-58;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRVILLMLFTAFPGILSDVQLQESGPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
DB 1 MRVILLMLFTAFPGILSDVQLQESGPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
QY 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQTSVTVSS 137
DB 121 TTAMDYWGQTSVTVSS 137
RESULT 2
ID ABB82796
XX ABB82796 standard; Protein; 134 AA.
AC ABB82796;
XX
DT 18-MAR-2003 (first entry)
XX
DE Antibody 806 variable heavy chain (VH) region.
XX
XX Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;
KW monoclonal antibody; mAb 806; antibody therapy; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /note= "signal peptide"
FT Protein 19..134
FT Protein /note= "mAb 806 VH region"
XX
PN WO200292771-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US15185.
XX
PR 11-MAY-2001; 2001US-290410P.
PR 28-SEP-2001; 2001US-326019P.
PR 21-DEC-2001; 2001US-342258P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX

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PI Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritter G;
PI Jungbluth A, Stockert E, Collins P, Cavenee WK, Huang H;
XX Burgess AW, Nice EC;
XX
DR WPI; 2003-129282/12.
DR N-PSDB; AB223940.
XX
XX Novel specific binding members, particularly antibodies recognizing
PT epidermal growth factor receptor epitope found only in tumorigenic
PT cells, useful for diagnosing, preventing and treating cancer in mammals
PT
PS Claim 6; Fig 14B; 123pp; English.
XX
XX The invention relates to an isolated specific binding member (I) which
CC recognizes an epidermal growth factor receptor (EGFR) epitope which is
CC found in tumorigenic, hyperproliferative or abnormal cells and not
CC detectable in normal cells. The EGFR epitope is located within the region
CC comprising residues 273-501 of EGFR and does not demonstrate any amino
CC acid sequence alterations or substitutions from normal EGFR. (I) is
CC capable of binding the de2-7 EGFR at an epitope distinct from the
CC junctional peptide and does not bind to EGFR on normal cells in the
CC absence of aberrant expression, or in the absence of amplification of
CC normal wild-type gene. The binding member comprises the VH and VL
CC polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for
CC treating or diagnosing human or animal body, especially for treating
CC tumour in a human. (I) is useful for the preparation of a medicament and
CC for preventing or treating cancer which is located in or adjacent the
CC brain, in a mammal. (I) is also useful for detecting the presence of
CC amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation, where
CC EGFR is measured by contacting a biological sample from a mammal in which
CC the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose
CC glycosylation is suspected with (I) under conditions that allow binding
CC of the EGFR to the antibody to occur, and detecting whether binding has
CC occurred between the EGFR from the sample and the antibody, where the
CC detection of binding indicates that presence or activity of the EGFR in
CC the sample. This method is useful for detecting cancer in mammals by
CC detecting the presence or activity of an EGFR which indicates the
CC existence of a tumour or cancer in the mammal. A pharmaceutical
CC composition comprising (I), and optionally vehicle, carrier or diluent is
CC useful for preventing and/or treating cancer in mammals, especially for
CC treating brain-resident cancers that produce aberrantly expressed EGFR in
CC mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic
CC astrocytoma or neoplastic arteriovenous malformations, and malignant
CC neural tumours in mammals. The present sequence represents the mAb 806
CC VH region.
XX
SQ Sequence 134 AA;
Query Match 82.7%; Score 593.5; DB 24; Length 134;
Best Local Similarity 83.9%; Pred. No. 1.8e-46;
Matches 115; Conservative 5; Mismatches 14; Indels 3; Gaps 1;
QY 1 MRVILLMLFTAFPGILSDVQLQESGPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
DB 1 MRVILLMLFTAFPGILSDVQLQESGPVLVKPSQSLTCTVTGYISITSDHAWSWIRQFP 60
QY 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWNGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQTSVTVSS 137
DB 118 GRGPPYWGQGLVTVSA 134
RESULT 3
AAB15672
ID AAB15672 standard; Protein; 136 AA.
XX
AC AAB15672;
XX
DT 08-JAN-2001 (first entry)

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XX DE Murine 5B3 antibody heavy chain variable region.
XX DE Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;
KW KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.
XX OS Mus sp.
XX FN WO200043774-A2.
XX PD 27-JUL-2000.
XX XX
XX XX 25-JAN-2000; 2000WO-IL00048.
XX PF
XX PR 25-JAN-1999; 99IL-0128212.
XX PA (YISS ) YISSUM RES & DEV CO.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX XX
XX PI Willner I, Eshhar Z;
XX XX
XX DR WPI; 2000-524259/47.
XX DR N-PSDB; AAA74604.
XX XX
XX PT Apparatus for detecting small molecules, especially explosives
XX PT comprises a piezoelectric crystal -
XX XX
XX PS Disclosure; Fig 3A; 90pp; English.
XX CC
XX CC The present sequence is the heavy chain variable region of 5B3 antibody.
XX CC The cDNA encoding this sequence was obtained from total RNA extracted
XX CC from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a
XX CC TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked
XX CC by very low amounts of TNT and it can therefore be used in a method for
XX CC detecting small assayed explosive molecules. Molecules are detected using
XX CC a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase
XX CC allows stationary and flow analysis of an aqueous sample. The method is
XX CC sufficiently sensitive for detection of low molecular weight molecules.
XX SQ
XX SQ Sequence 136 AA;
XX Query Match 81.9%; Score 588; DB 21; Length 136;
XX Best Local Similarity 83.8%; Pred. No. 5.8e-46;
XX Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;
Qy 1 MRVLILLWLTAFPGILSDVQLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFP 60
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 1 MRVLILLWLTAFPGILSDVQLQESGVLVKPSQSLTCTVTGYSITSGYAMWNIROFP 60
Qy 61 GNKLEWMGYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 61 GNKLEWMGYISYSGFTSNPSLSRISITRDTSKNQFFLQNSVTTSEDTATYYCARWDYG 120
Qy 121 TT--AMDYWGQGTSTV 134
Dy || || || || || || || || || || || || || || || || || || || || || ||
Dy 121 TTYGYFDVWGQGTTVT 136
XX RESULT 4
XX AAW01144
XX ID AAW01144 standard; Protein; 136 AA.
XX AC
XX AC AAW01144;
XX XX
XX DT 10-FEB-1997 (first entry)
XX DE
XX DE MAB 1.4 heavy chain, directed against type II phospholipase A2.
XX XX
XX XX Monoclonal antibody; phospholipase; myocardial infarction;
KW KW pancreatitis; cerebral infarction; acute kidney failure; colitis;
KW KW chronic rheumatism; adult respiratory distress syndrome;
XX XX cardiac shock; treatment; preclinical testing; disease; hybridoma.

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OS Mus musculus.
XX Key Location/Qualifiers
XX Binding-site 49..54
FT /label= CDR 1
FT Binding-site 69..84
FT /label= CDR 2
FT Binding-site 117..125
FT /label= CDR 3
XX XX
XX PN WO9620959-A1.
XX XX
XX PD 11-JUL-1996.
XX XX
XX PF 27-DEC-1995; 95WO-JP02714.
XX XX
XX PR 29-DEC-1994; 94JP-0340006.
XX XX
XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX XX
XX KA Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;
XX PI WPI; 1996-333946/33.
XX DR N-PSDB; AAT40804.
XX XX
XX PT Monoclonal antibody inhibiting type II phospholipase A2 activity -
XX PT for treatment of myocardial and cerebral infarction
XX XX
XX PS Claim 6; Figure 11; 69pp; Japanese.
XX CC
XX CC Monoclonal antibodies which inhibit type II phospholipase A2 are
XX CC useful in the treatment of myocardial infarction, cerebral
XX CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,
XX CC pancreatitis, adult respiratory distress syndrome and colitis. The
XX CC antibodies were generated by immunising Balb/C mice with recombinant
XX CC human type II phospholipase A2. Spleen cells from the mice were
XX CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas
XX CC obtained were screened for phospholipase A2 inhibitory activity.
XX CC Active clones were isolated including 12H5, 1.4 and 10.1. These
XX CC were cultured and the antibody isolated from the culture
XX CC supernatant by precipitation with ammonium sulphate and purification
XX CC on a column of protein A-Sepharose CL4B. Because the antibody acts
XX CC on the primate and mouse forms of enzyme as well as human it is
XX CC particularly suitable for preclinical testing.
XX SQ
XX SQ Sequence 136 AA;
XX Query Match 78.3%; Score 562.5; DB 17; Length 136;
XX Best Local Similarity 81.0%; Pred. No. 1.2e-43;
XX Matches 111; Conservative 6; Mismatches 19; Indels 1; Gaps 1;
Qy 1 MRVLILLWLTAFPGILSDVQLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFP 60
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 1 MRVLILLWLTAFPGILSDVQLQESGVLVKPSQSLTCTVTGYSITSDYAMWNIROFP 60
Qy 61 GNKLEWMGYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLAR 120
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 61 GNKLEWMGYIRYSGTYSNPSLKRISITRDTSONOFFLTLTSVTTEDTATYYCTRDLD 119
Qy 121 TTAMDYWGQGTSTVSS 137
Dy || || || || || || || || || || || || || || || || || || || || || ||
Dy 120 -AWYFDVWGAGTIVTSS 136
XX RESULT 5
XX AAW44169
XX ID AAW44169 standard; Protein; 136 AA.
XX XX
XX AC AAW44169;
XX XX
XX DT 16-JUN-1998 (first entry)
XX XX
XX DE Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.

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XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
KW amelioration; kidney disorder; nephrotoxicity; anticancer.
XX Unidentified.
OS WO9749427-A1.
PN 31-DEC-1997.
XX 27-JUN-1997; 97WO-JP02241.
XX 19-SEP-1996; 96JP-0247635.
PR 27-JUN-1996; 96JP-0167286.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;
XX WPI: 1998-076914/07.
DR N-PSDB; AAV12261.
XX Amelioration of kidney disorders caused by cisplatin administration
PT - by treatment with an antibody inhibiting type II phospholipase A2
PT activity
XX Disclosure; Page 38; 74pp; Japanese.
XX The present sequence represents the monoclonal antibody 1.4 heavy chain
CC against type II phospholipase A2, from the present invention. The
CC present invention describes a novel method for the amelioration of
CC kidney disorders (such as acute renal failure) associated with the
CC administration of cisplatin for the treatment of cancer. The method
CC comprises treatment with a monoclonal antibody which inhibits the
CC activity of type II phospholipase A2 (particularly of type II
CC phospholipase A2 of human origin), or with a protein or peptide
CC possessing the same inhibitory activity and containing a part of the
CC antibody sequence. Preferably the antibody also inhibits the activity of
CC ape and/or mouse type II phospholipase A2, and has the ability to
CC release type II phospholipase A2 bound to a cell membrane. Three
CC specific monoclonal antibodies having these properties which can be
CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,
CC FERM BP-5298 and FERM BP-5297 respectively. The method can be used for
CC suppressing the nephrotoxicity which is a characteristic feature of
CC cisplatin administration, and therefore allowing more efficient use of
CC this drug as an anticancer agent, e.g. by allowing an increased dosage
CC to be used.
XX Sequence 136 AA;
SQ
Query Match 78.3%; Score 562.5; DB 19; Length 136;
Best Local Similarity 81.0%; Pred. No. 1.2e-43;
Matches 111; Conservative 6; Mismatches 19; Indels 1; Gaps 1;
QY 1 MRVLLILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSIROPP 60
Db 1 MRVLLILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSIROPP 60
QY 61 GNKLEMMGYISYSGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSLAR 120
Db 61 GNKLEMMGYIRSYSGVTSYNPSLKSRISTRDTSKNQOFFLHLTSVTEDTATYCTRDLD 119
QY 121 TTAMDYWGQGTSTVTVSS 137
Db 120 AWYFDVWGAGTTVTVSS 136
RESULT 6
AAR29012
ID AAR29012 standard; Protein; 138 AA.
XX
AC AAR29012;
XX

DT 25-MAR-2003 (updated)
DT 30-MAR-1993 (first entry)
XX pUC-RVh-PW1f.
XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW complementarity determining region; mouse; monoclonal; hybridoma;
KW plasmid; polymerase chain reaction; amplify.
XX Synthetic.
OS
XX Location/Qualifiers
FH Key 1..19
FT Peptide /note= "Leader peptide"
FT Region 20..49
FT Region /label= FR1
FT Region 50..55
FT Region /label= CDR1
FT Region 56..69
FT Region /label= FR2
FT Region 70..85
FT Region /label= CDR2
FT Region 86..117
FT Region /label= FR3
FT Region 118..127
FT Region /label= CDR3
FT Region 128..138
FT Region /label= FR4
XX WO9219759-A1.
PN 12-NOV-1992.
PD
XX 24-APR-1992; 92WO-JP00544.
PR 25-APR-1991; 91JP-0095476.
PR 19-FEB-1992; 92JP-0032084.
XX (CHUS) CHUGAI SEIYAKU KK.
PA Bendig MM, Jones ST, Saidanha JW, Sato K, Tsuchiya M;
XX WPI: 1992-398882/48.
XX N-PSDB; AAQ31360.
DR Reconstituted human antibody to human interleukin-6 receptor -
XX has low antigenicity and contains mouse V-region complementarity
PT determining regions
PT Disclosure; Page 138-9; 207pp; Japanese.
XX The sequences given in AAR29012-15 are portions of monoclonal antibodies
CC which were encoded by plasmids derived from mouse hybridomas. The DNA
CC encoding complementarity determining regions (CDR's) was isolated by
CC polymerase chain reaction. These antibodies recognise human
CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC transformed with the plasmids encoding these genes which caused the
CC secretion of these antibodies from the hybridoma cells.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 138 AA;
SQ
Query Match 74.9%; Score 538; DB 13; Length 138;
Best Local Similarity 75.9%; Pred. No. 2.1e-41;
Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 5 ILLMLFTAPGILSDVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSIROPPGNKL 64
Db 6 ILLFVATATGVHQSQVQLQESGPGVLVPSQSLTCTVTGYSTSDHAWSVRQPPGRL 65
QY 65 EMGYISYSGITTYNPSLKSRISTRDTSKNQOFFLQLSNVTGDTSTYYCARSLARTAM 124
Db 66 EWIGVISYSGITTYNPSLKSRISTRDTSKNQOFFLRLSSVTAADTAVVYCARSLARTAM 125

QY 125 DYWGQGSTVTSS 137
 DB 126 DYWGQGSTVTSS 138

RESULT 7
 AAR29014
 ID AAR29014 standard; Protein; 138 AA.
 AC AAR29014;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-MAR-1993 (first entry)
 XX
 DE PUC-RVh-PM1f-4.
 XX
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
 KW complementarity determining region; mouse; monoclonal; hybridoma;
 KW plasmid; polymerase chain reaction; amplify.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /note= "Leader peptide"
 FT Region 20..49
 FT Region /label= FR1
 FT Region 50..55
 FT Region /label= CDR1
 FT Region 56..69
 FT Region /label= FR2
 FT Region 70..85
 FT Region /label= CDR2
 FT Region 86..117
 FT Region /label= FR3
 FT Region 118..127
 FT Region /label= CDR3
 FT Region 128..138
 FT Region /label= FR4
 XX
 PN WO9219759-A1.
 XX
 PD 12-NOV-1992.
 XX
 PP 24-APR-1992; 92WO-JP00544.
 XX
 PR 25-APR-1991; 91JP-0095476.
 PR 19-FEB-1992; 92JP-0032084.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 XX
 DR WPI; 1992-398882/48.
 DR N-PSDB; AAQ31365.
 XX
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 XX
 PS Disclosure; Page 142-3; 207pp; Japanese.
 XX
 CC The sequences given in AAR29012-15 are portions of monoclonal antibodies
 CC which were encoded by plasmids derived from mouse hybridomas. The DNA
 CC encoding complementarity determining regions (CDR's) was isolated by
 CC polymerase chain reaction. These antibodies recognise human
 CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
 CC transformed with the plasmids encoding these genes which caused the
 CC secretion of these antibodies from the hybridoma cells.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 138 AA;

Query Match 74.9%; Score 538; DB 13; Length 138;
 Best Local Similarity 75.9%; Pred. No. 2.1e-41;
 Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLFTAFPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRPPGNKL 64
 DB 6 IILFLVATATGVHSQVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRPPGNKL 65
 QY 65 EWMGYISYSGITTYNPSLKRISITRDTSKNOFFLQLSNVTTGDTSTVYCARSLARTTAM 124
 DB 66 EWIGYISYSGITTYNPSLKRVTMLRDTSKNOFSLRSLSSVTAADTAVYCARSLARTTAM 125
 QY 125 DYWGQGSTVTSS 137
 DB 126 DYWGQGSTVTSS 138

RESULT 8
 AAY55075
 ID AAY55075 standard; Protein; 260 AA.
 AC AAY55075;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Single chain Fv protein sequence shPW1(deltaEAL).
 XX
 KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX
 OS Synthetic.
 XX
 PN WO9960113-A1.
 XX
 PD 25-NOV-1999.
 XX
 PP 30-APR-1999; 99WO-JP02341.
 XX
 PR 20-MAY-1998; 98JP-0138652.
 PR 01-OCT-1998; 98JP-0279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Saito M, Ohtomo T;
 XX
 DR WPI; 2000-039382/03.
 DR N-PSDB; AAZ40305.
 XX
 PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein -
 XX
 PS Example 7; Page 80-82; 120pp; Japanese.
 XX
 CC This sequence represents a single chain Fv (ScFv) sequence.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC isolating the cDNA. The vector contains DNA encoding a secretable
 CC functional protein with antigenicity and binding affinity, and a cDNA
 CC ligated to DNA downstream of the 3' end of the coding sequence. The
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TWT) method
 CC wherein an epitope recognised by an antibody is carried in a fused
 CC protein.
 XX
 SQ Sequence 260 AA;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

```

QY 5 ILLWLFTAFPGLSDVQLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIROPPGNKL 64
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 IILFLVATATGVDQSQVLQESGVLVRPSQTLTCTVSGYSTSDHAWSWVRQPPGRGL 65
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 65 EWMGYISYGITTYNPSLKSRISTRDTSKNQFQLQNSVTGDTSTYYCARSARTAM 124
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 66 EWIGYISYGITTYNPSLKSRISTRDTSKNQFSLRLSSVTAADTAVVYCARSLARTAM 125
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 125 DYWGOGTSVTVSS 137
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 126 DYWGQGS�VTVSS 138
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

RESULT 11

AAV55080
ID AAY55080 standard; Protein; 519 AA.

XX AC AAY55080;

XX DT 25-FEB-2000 (first entry)

XX DE Single chain Fv protein sequence shPM1 (deltaEL)-BvGS3.

XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.

XX OS Synthetic.

XX PN WO9960113-A1.

XX PD 25-NOV-1999.

XX PF 30-APR-1999; 99WO-JP02341.

XX PR 20-MAY-1998; 98JP-0138652.

XX PR 01-OCT-1998; 98JP-0279876.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

XX DR N-PSDB; AAZ40312.

XX PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein

XX PS Example 7; Page 95-100; 120pp; Japanese.

XX CC This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.

XX SQ Sequence 519 AA;

Query Match 74.8%; Score 537; DB 21; Length 519;

Best Local Similarity 75.9%; Pred. No. 1.1e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

```

QY 5 ILLWLFTAFPGLSDVQLQESGVLVKPSQSLTCTVTGYSTSDHAWSWIROPPGNKL 64
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 IILFLVATATGVDQSQVLQESGVLVRPSQTLTCTVSGYSTSDHAWSWVRQPPGRGL 65
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 65 EWMGYISYGITTYNPSLKSRISTRDTSKNQFQLQNSVTGDTSTYYCARSARTAM 124
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 66 EWIGYISYGITTYNPSLKSRISTRDTSKNQFSLRLSSVTAADTAVVYCARSLARTAM 125
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 125 DYWGOGTSVTVSS 137
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 126 DYWGQGS�VTVSS 138
   :|:|:|:|:|:|:|:|:~|:|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|

```

RESULT 12

AAV55074
ID AAY55074 standard; Protein; 546 AA.

XX AC AAY55074;

XX DT 25-FEB-2000 (first entry)

XX DE Single chain Fv protein sequence hPM1-BvGS3.

XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.

XX OS Synthetic.

XX PN WO9960113-A1.

XX PD 25-NOV-1999.

XX PF 30-APR-1999; 99WO-JP02341.

XX PR 20-MAY-1998; 98JP-0138652.

XX PR 01-OCT-1998; 98JP-0279876.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

XX DR N-PSDB; AAZ40303.

XX PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein

XX PS Example 5; Page 73-78; 120pp; Japanese.

XX CC This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.

XX SQ Sequence 546 AA;

Query Match 74.8%; Score 537; DB 21; Length 546;

Best Local Similarity 75.9%; Pred. No. 1.2e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLSLTCTVTGYSITSDHAWSWIRQPPGNKL 64
 Db 6 IILFLVATATGVDVQVQLQESGPGVLVRSQTLISLCTVSGYSITSDHAWSWIRQPPGRGL 65
 QY 65 EWMGYISYSGITTYNPSLKSRISTRDTSKNOFFLOLNSVTTGDTSTYYCARSARTTAM 124
 Db 66 EWIGYISYSGITTYNPSLKSRISTRDTSKNOFFLOLNSVTTGDTSTYYCARSARTTAM 125
 QY 125 DYWGOGTSVTVSS 137
 Db 126 DYWGQGS�VTVSS 138

RESULT 13

AY55081
 ID AAY55081 standard; Protein; 626 AA.
 XX AC AAY55081;
 XX DT 25-FEB-2000 (first entry)
 XX DE Single chain Fv protein sequence sHPM1-kappa-BvGS3.
 XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secreted functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX OS Synthetic.
 XX PN WO9960113-A1.
 XX PD 25-NOV-1999.
 XX PF 30-APR-1999; 99WO-JP02341.
 XX PR 20-MAY-1998; 98JP-0138652.
 PR 01-OCT-1998; 98JP-0279876.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Saito M, Ohtomo T;
 DR WPI; 2000-039382/03.
 DR N-PSDB; AA240316.
 XX PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein -
 XX Example 7; Page 103-109; 120pp; Japanese.
 PS
 XX CC This sequence represents a single chain Fv (ScFv) sequence.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC isolating the cDNA. The vector contains DNA encoding a secreted
 CC functional protein with antigenicity and binding affinity, and a cDNA
 CC ligated to DNA downstream of the 3' end of the coding sequence. The
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TWT) method
 CC wherein an epitope recognised by an antibody is carried in a fused
 CC protein.
 XX SQ Sequence 626 AA;

Query Match 74.8%; Score 537; DB 21; Length 626;

Best Local Similarity 75.9%; Pred. No. 1.4e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLSLTCTVTGYSITSDHAWSWIRQPPGNKL 64

Db 6 IILFLVATATGVDVQVQLQESGPGVLVRSQTLISLCTVSGYSITSDHAWSWIRQPPGRGL 65
 QY 65 EWMGYISYSGITTYNPSLKSRISTRDTSKNOFFLOLNSVTTGDTSTYYCARSARTTAM 124
 Db 66 EWIGYISYSGITTYNPSLKSRISTRDTSKNOFFLOLNSVTTGDTSTYYCARSARTTAM 125
 QY 125 DYWGOGTSVTVSS 137
 Db 126 DYWGQGS�VTVSS 138

RESULT 14

AY55082
 ID AAY55082 standard; Protein; 640 AA.
 XX AC AAY55082;
 XX DT 25-FEB-2000 (first entry)
 XX DE Single chain Fv protein sequence sHPM1-MCH4-BvGS3.
 XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secreted functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX OS Synthetic.
 XX PN WO9960113-A1.
 XX PD 25-NOV-1999.
 XX PF 30-APR-1999; 99WO-JP02341.
 XX PR 20-MAY-1998; 98JP-0138652.
 PR 01-OCT-1998; 98JP-0279876.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Saito M, Ohtomo T;
 DR WPI; 2000-039382/03.
 DR N-PSDB; AA240321.
 XX PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein -
 XX Example 7; Page 111-117; 120pp; Japanese.
 PS
 XX CC This sequence represents a single chain Fv (ScFv) sequence.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC isolating the cDNA. The vector contains DNA encoding a secreted
 CC functional protein with antigenicity and binding affinity, and a cDNA
 CC ligated to DNA downstream of the 3' end of the coding sequence. The
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TWT) method
 CC wherein an epitope recognised by an antibody is carried in a fused
 CC protein.
 XX SQ Sequence 640 AA;

Query Match 74.8%; Score 537; DB 21; Length 640;

Best Local Similarity 75.9%; Pred. No. 1.4e-40;

Matches 101; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 ILLWLTAPPGLSDVQLQESGVLVVKPSQSLSLTCTVTGYSITSDHAWSWIRQPPGNKL 64

Db	6	IILFLVATATGVD	SOVQLQESPG	LVRPSQTL	SLTCTV	SGYSITSD	HANSWVRQPP	CGSL	65	
Qy	65	ENWGIISYSGI	ITYNP	SLKSRIS	TRDTSK	NQKQFL	QLNSVT	TGDTST	YICARSLARTTAM	124
Db	66	EWIGIISYSGI	ITYNP	SLKSRVT	MLRDTSK	NQKQFL	SLRSVT	TAADTAV	YICARSLARTTAM	125
Qy	125	DYWGQGS	TVTSS	137						
Db	126	DYWGQGS	TVTSS	138						

RESULT 15

AAW01584
ID AAW01584 standard; Protein; 119 AA.

AA AAW01584;

DT 22-AUG-1997 (first entry)

DE . Lead binding MAb 13D10 heavy chain variable region.

Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
pharmaceutical; health care; skin treatment; pesticide; herbicide;
heavy metal.

XX
QS
MUS MUSCULUS

XX
PN
WO9639518-A1XX
PD
12-DEC-1996XX
DE 05-JUN-1996.XX
DB 10-OCT-1995. 05118-0541373

PR 05-JUN-1995; 95US-0462798.

PA (BION-) BIONEBRASKA INC.

PI Lopez O, Murray PJ, Wy

DR WPI; 1997-043140/04.

DR N-PSDB; AA1304238.
XX

PT DNA encoding heavy
PT detecting removing

PT
lead cations
yy

PS Claim 12; Page 71; 125pp; English.

The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 13D10, which immunoreacts with a lead cation. The sequence was derived from DNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.

AA	Sequence	119 AA;
SQ		

Query Match	74.4%	Score 534;	DB 18;	Length 119;
Best Local Similarity	85.7%	Pred. No. 4.1e-41;		
Matches 102; Conservative		6; Mismatches 11;	Indels 0;	Gaps 0;

Qy	19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLENWGYISYSGITT Y 78 : : : : : : : : :
Dd	1 DVQLQESGPLVKPSQSLSLTCTVTGYSITS DYAWNWIROFPGNKLENNWGYISYSGSTSY 60 : : : : : : : : :

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:50 ; Search time 25.947 Seconds
(without alignments)
507.771 Million cell updates/sec

Title: US-09-114-285A-31
Perfect score: 718
Sequence: 1 MRVLLILWLFTAPFGILSDV.....LARTAMDYWGQTSVTSS 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	603.5	84.1	135	2 PLO100	Ig heavy chain pre
2	593	82.6	149	2 S30752	Ig heavy chain pre
3	585.5	78.8	134	2 S24672	Ig heavy chain pre
4	543	75.6	116	1 HVMS1B	Ig heavy chain pre
5	538	74.9	137	1 AVMS35	Ig heavy chain pre
6	536	74.7	119	2 CS3285	Ig heavy chain v r
7	532	74.1	117	2 I28195	Ig heavy chain v r
8	520.5	72.5	116	2 S38718	Ig heavy chain v r
9	519.5	72.4	136	2 S07637	Ig heavy chain v r
10	517.5	72.1	114	2 T01262	Ig heavy chain v r
11	510	71.0	116	1 HVMS31	Ig heavy chain pre
12	486	67.7	121	2 S37200	Ig heavy chain v r
13	479	66.7	119	2 E25114	Ig heavy chain v r
14	478.5	66.6	106	2 S26464	Ig heavy chain v r
15	477.5	66.5	115	2 D33932	Ig mu chain precu
16	476	66.3	117	2 I57810	gene C72-3A1 prote
17	474	66.0	119	2 C25114	Ig heavy chain v r
18	467	65.0	106	2 S59639	Ig heavy chain v r
19	466.5	65.0	120	2 A25114	Ig heavy chain v r
20	461.5	64.3	117	1 HVMS73	Ig heavy chain pre
21	455	63.4	123	2 S42771	Ig heavy chain - m
22	453	63.1	115	2 F25114	Ig heavy chain v r
23	450	62.7	113	1 G2MS60	Ig heavy chain v r
24	445	62.0	119	2 D25114	Ig heavy chain v r
25	433.5	60.4	104	2 S26467	Ig heavy chain v r
26	423	58.9	140	2 I37782	Ig variable region
27	419.5	58.4	100	2 S14485	Ig heavy chain v r
28	416.5	58.0	102	2 S14488	Ig heavy chain v r
29	414.5	57.7	101	2 S14484	Ig heavy chain v r

30 414.5 57.7 155 2 S31511 Ig heavy chain - h
31 412.5 57.5 155 2 S31512 Ig heavy chain - h
32 408 56.8 147 2 S13519 Ig heavy chain v r
33 407 56.7 130 2 S31690 Ig heavy chain v r
34 406.5 56.6 102 2 S14486 Ig heavy chain v r
35 405 56.4 146 2 S09711 Ig heavy chain v r
36 404.5 56.3 137 2 S31676 Ig heavy chain v r
37 402 56.0 102 2 S14487 Ig heavy chain v r
38 399.5 55.6 141 2 S54236 Ig mu heavy chain
39 395.5 55.1 145 2 S78055 Ig heavy chain pre
40 394.5 54.9 139 2 S31586 Ig heavy chain v r
41 394 54.9 123 2 S30530 Ig heavy chain v r
42 394 54.9 135 2 S78051 Ig heavy chain pre
43 394 54.9 139 2 A32456 Ig heavy chain pre
44 391.5 54.5 143 2 S54249 Ig mu heavy chain
45 391 54.5 112 2 S13685 Ig heavy chain v r

ALIGNMENTS

RESULT 1

PL0100
Ig heavy chain precursor V region (40-140) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0100
R:Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A:Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A:Reference number: PL0100; MUID:89238344; PMID:2497340
A:Accession: PL0100
A:Molecule type: DNA
A:Residues: 1-135 <NEA>
A:Cross-references: GB:M27660; NID:G341745; PIDN:AAA58746.1; PID:G609530
A:Experimental source: strain A/J
A:Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family
C:Genetics:
A:Introns: 15/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-115/Domain: V segment #status predicted <VRE>

F:33-116/Domain: immunoglobulin homology <IMM>

F:117-118/Domain: D segment #status predicted <DRE>

F:119-135/Domain: J segment #status predicted <JRE>

Query Match 84.1%; Score 603.5; DB 2; Length 135;

Best Local Similarity 84.7%; Pred. No. 9.9e-46;

Matches 116; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MRVLLILWLFTAPFGILSDVQLQESGVLKPSQSLTCTVTCGYSITSDHAWSWIRQFP 60

Db 1 MRVLLILWLFTAPFGILSDVQLQESGVLKPSQSLTCTVTCGYSITSDHAWSWIRQFP 60

Qy 61 GNKLEWNGYISYSGITTYNPSLKSRIITRDTSKNQFFLQNLNSVTGDTSTYYCARSLAR 120

Db 61 GNKLEWNGYITNGYTYNPSLKSRIITRDTSKNQFLQLSSVTTEDATYYCARSY-- 118

Qy 121 TTAMDYWGQTSVTSS 137

Db 119 -DYFDYWGQTTLTSS 134

RESULT 2

S30752

Ig heavy chain precursor V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C:Accession: S30752

R:Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.

Nucleic Acids Res. 15, 5496, 1987

A:Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C:Accession: I28195
J:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: I28195
A:Molecule type: mRNA
A:Residues: 1-117 <SHE>
A:Cross-references: GB:MI9775; NID:G195526; PIDN:AAA38343.1; PID:G195527
A:Note: the authors translated the codon AAC for residue 61 as Thr, and did not translate
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 532; DB 2; Length 117;
Best Local Similarity 85.7%; Pred. No. 1.4e-39;
Matches 102; Conservative 67; Mismatches 9; Indels 2; Gaps 1;

Qy 19 DVLOEGSPVLVQPSQSLSLCTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYGITTY 78
Db 1 DVLOEGSPGLVQPSQSLSLCTCTVTGYGITSSEYANNWIRQFPGNKLEWNGYISYSGTTSY 60

Qy 79 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLKTRISITRDTSKNOFFLQLNSVTTEDTATYYCARD--NGNCGDYWGQGTSTVTVSS 117

RESULT 8
S38718
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38718
F:Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38718
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <CIM>
A:Cross-references: EMBL:X76018; NID:G416102; PIDN:CAA53605.1; PID:G1334263
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 520.5; DB 2; Length 116;
Best Local Similarity 84.0%; Pred. No. 1.4e-38;
Matches 100; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

Qy 19 DVLOEGSPVLVQPSQSLSLCTCTVTGYGITSDDHAMSWIRQFPGNKLEWNGYISYGITTY 78
Db 1 DVLOEGSPGLVQPSQSLSLCTCAVTGYGITSDYANNWIRQFPGNKLEWNGYISYGTINY 60

Qy 79 NPSLKRSISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLKRSISITRDTSKNOFFLQLNSVTTEDTATYYCARG--GTGFTFWGQGTLTIVSA 116

RESULT 9
S07637
Ig heavy chain V region (PTF.02) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S07637
R:Urakov, D.N.; Deev, S.M.; Polyakovskiy, O.L.
Nucleic Acids Res. 17, 9481, 1989
A:Title: The structure of the expressible VH gene from a hybridoma producing monoclonal
A:Reference number: S07637; MUID:90067954; PMID:2587273
A:Accession: S07637
A:Molecule type: DNA
A:Residues: 1-136 <URA>

Qy 61 GNKLEWVGYSYSGIITTYNPSLKRSISIRDTSKNQFFQLNSVTGDTSTYYCAR 116
|||||:||||||| |||||||||:||:|||||
Dd 60 GNKLEYMGYSYSGSTYNPSLKRSISIRDTSKNOYVQLNSVTTEDTATYYCAR 115

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:20 ; Search time 14.0114 Seconds
(without alignments)
459.817 Million cell updates/sec

Title: US-09-114-285a-31

Perfect score: 718

Sequence: 1 MRVLLILWLFTAFPGILSDV.....LARTAMDYMGQTSVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	75.6	116	1 HV61_MOUSE	P18532 mus musculus
2	538	74.9	137	1 HV46_MOUSE	P18822 mus musculus
3	510	71.0	116	1 HV60_MOUSE	P18531 mus musculus
4	461.5	64.3	117	1 HV62_MOUSE	P18533 mus musculus
5	450	62.7	113	1 HV47_MOUSE	P18823 mus musculus
6	384.5	53.6	144	1 HV43_MOUSE	P1819 mus musculus
7	377.5	52.6	146	1 HV21_HUMAN	P06331 homo sapien
8	338	47.1	135	1 HV02_XENLA	P20957 xenopus lae
9	337	46.9	117	1 HV2G_HUMAN	P18825 homo sapien
10	330	46.0	115	1 HV44_MOUSE	P18820 mus musculus
11	328	45.7	129	1 HV2F_HUMAN	P18824 homo sapien
12	323	45.0	121	1 HV2E_HUMAN	P1818 homo sapien
13	316	44.0	116	1 HV45_MOUSE	P18821 mus musculus
14	312.5	43.5	136	1 HV01_XENLA	P20956 xenopus lae
15	308	42.9	119	1 HV2C_HUMAN	P1816 homo sapien
16	295.5	41.2	147	1 HV2H_HUMAN	P04438 homo sapien
17	295	41.1	125	1 HV2D_HUMAN	P1817 homo sapien
18	291.5	40.6	120	1 HV2B_HUMAN	P1815 homo sapien
19	285.5	40.3	136	1 HV16_MOUSE	P18783 mus musculus
20	287.5	40.0	139	1 HV07_MOUSE	P1751 mus musculus
21	287	40.0	140	1 HV02_MOUSE	P1746 mus musculus
22	285.5	39.8	137	1 HV11_MOUSE	P1755 mus musculus
23	280	39.0	115	1 HV3F_HUMAN	P1767 homo sapien
24	278.5	38.8	122	1 HV3H_HUMAN	P1769 homo sapien
25	277.5	38.6	126	1 HV3A_HUMAN	P1814 homo sapien
26	277	38.6	119	1 HV3L_HUMAN	P1773 homo sapien
27	276.5	38.5	122	1 HV3G_HUMAN	P1768 homo sapien
28	276	38.4	117	1 HV13_MOUSE	P1757 mus musculus
29	274	38.2	117	1 HV17_MOUSE	P1786 mus musculus
30	274	38.2	136	1 HV15_MOUSE	P1759 mus musculus
31	273	38.0	120	1 HV03_MOUSE	P1747 mus musculus
32	272	37.9	117	1 HV42_MOUSE	P1812 mus musculus
33	272	37.9	121	1 HV3J_HUMAN	P1771 homo sapien

34	272	37.9	142	1 HV01_RAT	P01805 rattus norv
35	271	37.7	117	1 HV12_MOUSE	P01756 mus musculus
36	266.5	37.1	122	1 HV3A_HUMAN	P01762 homo sapien
37	266.5	37.1	126	1 HV3K_HUMAN	P01772 homo sapien
38	265.5	37.0	119	1 HV40_MOUSE	P01810 mus musculus
39	265	36.9	117	1 HV14_MOUSE	P01758 mus musculus
40	264.5	36.8	116	1 HV31_HUMAN	P01781 homo sapien
41	264.5	36.8	118	1 HV51_MOUSE	P06330 mus musculus
42	264.5	36.8	119	1 HV38_MOUSE	P01808 mus musculus
43	262	36.5	117	1 HV3C_HUMAN	P01764 homo sapien
44	262	36.5	117	1 HV41_MOUSE	P01811 mus musculus
45	262	36.5	117	1 HV54_MOUSE	P18525 mus musculus

ALIGNMENTS

RESULT 1
ID HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR; JTO508; HVMS1B.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 75.6%; Score 543; DB 1; Length 116;
Best Local Similarity 90.5%; Pred. No. 7e-46;
Matches 105; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MRVLLILWLFTAFPGILSDVQLQESGVLKPKSLSLTCTVTCTSYITSDHAWSIROFP	60
Db	1	MRVLLILWLFTAFPGILSDVQLQESGVLKPKSLSLTCTVTCTSYITSDHAWSIROFP	60
Qy	61	GNKLEWNGYISYSGITTYNPNLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCAR	116
Db	61	GNKLEWNGYIHYSGNTSYNPNLSKRSITRDTSKNQFFLQLNSVTGDTSTYYCAR	116

RESULT 2


```
QY 1 MRVLLILLWLTAFPGILSDVQLQSGPVLVKPQSLSLTCTVTGYSITSDHAWSWIRQFP 60
Db 1 MKVLSLLYLLTAIPGILSDVQLQSGPGLVKPQSLSLTCTVTGYSITSGTYNWMIRQFP 60
QY 61 GNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
Db 61 GNKLEWMCYISYDGSNNYNPSLKNRISITRDTSKNQFFLQNSVTTEDTATYYCAR 116

RESULT 4
HV62 MOUSE
ID HV62 MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 733 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J070510; HVMS73.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 64.3%; Score 461.5; DB 1; Length 117;
Best Local Similarity 74.4%; Pred. No. 5.4e-38;
Matches 87; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 MRVLLILLWLTAFPGILSDVQLQSGPVLVKPQSLSLTCTVTGYSITSDHAWSWIRQFP 59
Db 1 MKMFTLLYLLTVPGILSDVQLQSGPGLVKPQSLSLTCTVTGYSITSGTYNWMIRQFP 60
QY 60 PNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCAR 116
Db 61 PNKLEWMCYISYSAITSYNPSKRSRTITRDTSKNQFFLEWNSLTAEEDTATYYCAR 117

RESULT 5
HV47 MOUSE
ID HV47 MOUSE STANDARD; PRT; 113 AA.
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 36-60.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
```

```
RC STRAIN=A/J;
RX MEDLINE=84024551; PubMed=6414509;
RA Juszcak E.C., Margolies M.N.;
RT "Amino acid sequence of the heavy chain variable region from the A/J
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
RT idio type.";
RL Biochemistry 22:4291-4296(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC STRAIN A/J MICE.
DR PIR; A02098; G2MS60.
DR PDB; 1J10; 18-FEB-03.
DR PDB; 1J1P; 18-FEB-03.
DR PDB; 1J1X; 18-FEB-03.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

Query Match 62.7%; Score 450; DB 1; Length 113;
Best Local Similarity 74.8%; Pred. No. 6.8e-37;
Matches 89; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

QY 19 DVQLQESGPVLVKPQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMCYISGITYY 78
Db 1 EVQLQESGPVLVKPQSLSLTCTSVTGSITSDY-WNNIRKFPGNKLEHMGYISYSGTYY 59
QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTTAMDVWGQTSVTYSS 137
Db 60 NPSLKRISITRDTSKNQYLLQNSVTSDEDTATYYCT-----SURFAYWGQTLVTVSA 113

RESULT 6
HV43 MOUSE
ID HV43 MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
```

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 53.6%; Score 384.5; DB 1; Length 144;
Best Local Similarity 56.2%; Pred. No. 2e-30;
Matches 82; Conservative 22; Mismatches 31; Indels 11; Gaps 4;

QY 1 MRVLILLMLFTAPPG-ILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
Db 1 MAVLALLFLCLATPPSCILSQVLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
QY 60 PGNKLEWGWYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCA---- 115
Db 60 PKGLEWLTGNGSTDYNSLTKRLTITKNSQVFLKMSLQTDRTARYCASVSI 119
QY 116 ----RSLARTTAMDYWGQGSTVTSS 137
Db 120 YYGRS-DKYFLDYWGQGSTVTSS 144

RESULT 7
HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.;
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RL repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR: A02101; GIH02.
DR HSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 127 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 52.6%; Score 377.5; DB 1; Length 146;
Best Local Similarity 56.7%; Pred. No. 9.5e-30;
Matches 80; Conservative 16; Mismatches 36; Indels 9; Gaps 2;

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 53.6%; Score 384.5; DB 1; Length 144;
Best Local Similarity 56.2%; Pred. No. 2e-30;
Matches 82; Conservative 22; Mismatches 31; Indels 11; Gaps 4;

QY 1 MRVLILLMLFTAPPG-ILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
Db 1 MAVLALLFLCLATPPSCILSQVLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQF 59
QY 60 PGNKLEWGWYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCA---- 115
Db 60 PKGLEWLTGNGSTDYNSLTKRLTITKNSQVFLKMSLQTDRTARYCASVSI 119
QY 116 ----RSLARTTAMDYWGQGSTVTSS 137
Db 120 YYGRS-DKYFLDYWGQGSTVTSS 144

RESULT 8
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.;
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib.ch).
CC EMBL: J03632; AAA49791.1; -
CC PIR: B31933; B31933.
CC HSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-Like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 47.1%; Score 338; DB 1; Length 135;
Best Local Similarity 50.7%; Pred. No. 5.7e-26;
Matches 68; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

QY 5 ILLWLTAF-PGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNK 63
Db 3 IIFIFWFFSPCILSQVLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPGNK 61
QY 64 LEWNGYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTTGDTSTYYCARSLARTTA 123
Db 62 LEWIGVATGGSTAIDSLKNRVITTKDNGKKQVQLQNGMEVKDTAMYYCAREYASGYN 121
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RP SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RR Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -!- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02093; GIHUHE.
CC HSSP; P01825; 7FAB.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunglobulin V region; Pyrolidone carboxylic acid.
CC DOMAIN 1 120
CC MOD_RES 1 1
CC NON_TER 121 121
CC SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 45.0%; Score 323; DB 1; Length 121;
Best Local Similarity 52.5%; Pred.No. 1.4e-24;
Matches 63; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 20 VOLESQPVLVKPSQSLSTCTVTGYSITSDH-AMSWIRQFFGNKLEWNGYISY-SGITT 77
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2 VTLKENGPLVLPKPTETLTCTLSGLSLTDTGVAVGWIRQGGRALEWLAWLLYWDKKR 61

QY 78 YNPSLKSRISITRDTSKNOFFQLQNSVTTGDTSTTYCARSLARTTAMDYWGQSTSVVSS 137
DB ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 FSPSLKSRILVTRDTSKNQVLTMTNMDPVDATTYCVHRHPTLAFDVGWGQTKVAVSS 121

RESULT 13
ID HV45_MOUSE STANDARD; PRT; 116 AA.
AC P01821;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MC101 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=82075900; PubMed=6273429;
Kataoka T., Nikaïdo T., Miyata T., Moriwaki K., Honjo T.;
"The nucleotide sequences of rearranged and germ-line immunoglobulin
VH genes of a mouse myeloma MC101 and evolution of VH genes in
mouse.";
J. Biol. Chem. 257:277-285(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00502; AAA38515.1; -.
CC PIR; A02096; GIMS10.
CC HSSP; P01772; 2FB4.
CC InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.
FT DOMAIN 20 >116 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

Query Match 44.0%; Score 316; DB 1; Length 116;
Best Local Similarity 53.8%; Pred. No. 6.5e-24;
Matches 63; Conservative 22; Mismatches 30; Indels 2; Gaps 2;

QY 1 MRVLILLWLFAPFG-IISDVLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROF 59
Db 1 MAVLGLLFLVTFPCVLISQVQLKOSGGLVQPSQSLTCTVTGYSITSDHAWSWIROF 59
QY 60 PGNKLEWNGYISGITTYPNPSLKRISITRDTSKNQFFLQNSVTTGDTSTTYCAR 116
Db 60 PKGLEWLGVIWGGSTDYNAAFISRLSISKNSKQVFFKXNSLQSNDAIYYCAR 116

RESULT 14
HV01 XENLA
ID HV01 XENLA STANDARD; PRT; 136 AA.
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG8 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced from cDNA sequence: implications for evolution of immunoglobulin domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; M20484; AAA49774.1; ALT_TERM.
DR PIR; A31933; A31933.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT DOMAIN 19 128 IG-LIKE.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match 43.5%; Score 312.5; DB 1; Length 136;
Best Local Similarity 47.4%; Pred. No. 1.7e-23;
Matches 64; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 4 LILLWLFAPGILSDVLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFGNK 63
Db 4 IFVIMFSPSCILSQT-LQESGGTVKPSLSLCTVSGFELTSYVY-WIQPPRKT 61
QY 64 LEWNGYISGITTYPNPSLKRISITRDTSKNQFFLQNSVTTGDTSTTYCARSLRTTA 123
Db 62 LEWIGVVRTDGTSTAIADSLKNRVTITKDNCKQVYLQWNGMEVKDTAMYYCTSLAGTAG 121

QY 124 -MDYWGOGTSVTSS 137
Db 122 YFEHWGQGTMTVTS 136

RESULT 15
HV2C HUMAN
ID HV2C HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1 heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; G1HUDW.
DR HSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 42.9%; Score 308; DB 1; Length 119;
Best Local Similarity 50.4%; Pred. No. 4e-23;
Matches 60; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

QY 20 VLQESGVLVKPSQSLTCTVTGYSITSDHAWSWIROFGNKLEWNGYISGITY 78
Db 2 VTLRESGPAVLRPTQLTCTFSGSLSGTMCVAMIRQPPGGALEWLNDLDDKY 61
QY 79 NPSLKRISITRDTSKNQFFLQNSVTTGDTSTTYCARSLRTTAMDYWGOGTSVTSS 137
Db 62 GASLETRAVSKDTSKNQVLLSMNTVPGDGTATYCARSCG-SQYFDYWGQGLVTS 119

Search completed: October 22, 2003, 22:17:09
Job time : 14.0114 secs
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:13:15 ; Search time 62.7917 Seconds
(without alignments)
563.024 Million cell updates/sec

Title: US-09-114-285A-31
Perfect score: 718
Sequence: 1 MRVLILLWLTAPFGILSDV.....LARTTAMYGQGTSTVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	531	74.0	479	11 Q99M22	Q99M22 mus musculus
2	414	57.7	482	11 Q91X92	Q91X92 mus musculus
3	393.5	54.8	496	4 Q96KX8	Q96KX8 homo sapien
4	386.5	53.8	613	4 Q96EY0	Q96EY0 homo sapien
5	382	53.2	119	4 Q9UL73	Q9UL73 homo sapien
6	374.5	52.2	150	4 Q95973	Q95973 homo sapien
7	374	52.1	597	4 Q9BQ88	Q9BQ88 homo sapien
8	368	51.3	588	4 Q9WUX4	Q9WUX4 homo sapien
9	368	51.3	597	4 Q9BU10	Q9BU10 homo sapien
10	368	51.3	618	4 Q96AA6	Q96AA6 homo sapien
11	367.5	51.2	121	11 Q99NG4	Q99NG4 mus musculus
12	359.5	50.1	122	4 Q9UL75	Q9UL75 homo sapien
13	336.5	46.9	473	4 Q8TC63	Q8TC63 homo sapien
14	328.5	45.8	130	4 Q8IZD7	Q8IZD7 homo sapien
15	313	43.6	121	4 Q9UL96	Q9UL96 homo sapien
16	312	43.5	468	11 Q99L31	Q99L31 mus musculus

17	310.5	43.2	488	11 Q91WR1	Q91WR1 mus musculus
18	307.5	42.8	487	11 Q99KA4	Q99KA4 mus musculus
19	304	42.3	117	11 Q9QXE9	Q9QXE9 mus musculus
20	303	42.2	597	4 Q96BB9	Q96BB9 homo sapien
21	300.5	41.9	613	11 Q8VCX7	Q8VCX7 mus musculus
22	298.5	41.6	482	11 Q8K172	Q8K172 mus musculus
23	298.5	41.6	573	4 Q8WU38	Q8WU38 homo sapien
24	297.5	41.4	473	11 Q91Z05	Q91Z05 mus musculus
25	296.5	41.3	145	11 Q924Q9	Q924Q9 mus musculus
26	296.5	41.3	469	11 Q8R3V9	Q8R3V9 mus musculus
27	293	40.8	484	11 Q99LA6	Q99LA6 mus musculus
28	292.5	40.7	145	11 Q924Q6	Q924Q6 mus musculus
29	292.5	40.7	471	4 Q8TC77	Q8TC77 homo sapien
30	292.5	40.7	613	4 Q8WUK1	Q8WUK1 homo sapien
31	291	40.5	499	4 Q8NSK4	Q8NSK4 homo sapien
32	290	40.4	131	4 Q9UL88	Q9UL88 homo sapien
33	289	40.3	118	4 Q9UL74	Q9UL74 homo sapien
34	288	40.1	146	11 Q924Q3	Q924Q3 mus musculus
35	287	40.0	142	11 Q924Q1	Q924Q1 mus musculus
36	286.5	39.9	118	4 Q9UL91	Q9UL91 homo sapien
37	286	39.8	168	11 Q8VDC9	Q8VDC9 mus musculus
38	285.5	39.8	481	11 Q8VCV5	Q8VCV5 mus musculus
39	285	39.7	117	11 Q9QXF0	Q9QXF0 mus musculus
40	285	39.7	119	11 Q920E7	Q920E7 mus musculus
41	284.5	39.6	241	11 Q921A6	Q921A6 mus musculus
42	284.5	39.6	484	11 Q8VEA0	Q8VEA0 mus musculus
43	284	39.6	113	4 Q9UL90	Q9UL90 homo sapien
44	284	39.6	480	11 Q91XE1	Q91XE1 mus musculus
45	283.5	39.5	145	11 Q924R4	Q924R4 mus musculus

ALIGNMENTS

RESULT 1

Q99M22	ID	Q99M22	PRELIMINARY;	PRT;	479 AA.
AC	Q99M22;				
DT	01-JUN-2001	(Tremblrel. 17, Created)			
DT	01-JUN-2001	(Tremblrel. 17, Last sequence update)			
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)			
DE	Hypothetical 52.0 kDa protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Strausberg R.;				
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC002091; AAH02091.1; -				
DR	HSSP; P01810; 2FEJ.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 4.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; 2.				
KW	Hypothetical protein.				
SQ	SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;				

Query Match	74.0%	Score 531;	DB 11;	Length 479;
Best Local Similarity	73.9%;	Pred. No. 3.8e-46;		
Matches 105;	Conservative 11;	Mismatches 14;	Indels 12;	Gaps 2;
Qy	1	MRVLILLWLTAPFGILSDVQLQESGVLVKPQSLSLTCTVTGYSITSDHAWSWIRQFP	60	
Db	1	MKVLSSLYLTLTAPGILSDVQLQESGVLVKPQSLSLTCTVTGYSITSGYNNWIRQFP	60	
Qy	61	GNKLEWNGYISYGITTYNPNLSKRSITRDTSKNQFFLQNLNSVTGDTFTYYCARSLAR	120	
Db	61	GNKLEWNGYINYGNNYNNPNLSKRSITRDTSKNQFFLQNLNSVTGDTFTYYCARSLAR	115	

QY 121 TTAMDY----WGQGTSTVTVSS 137
 Db 116 --SRGYSWFPNWGQGLTVTVSA 135

RESULT 2

Q91X92 PRELIMINARY; PRT; 482 AA.
 AC Q91X92; 7 LWF-...TAPP-GILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 61
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Unknown (Protein for MGC:18822).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011181; AAH1181.1; -.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 57.7%; Score 414; DB 11; Length 482;

Best Local Similarity 60.9%; Pred. No. 4e-34;
 Matches 84; Conservative 19; Mismatches 33; Indels 2; Gaps 2;

QY 1 MRVLLLLWLTAPPG-ILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQF 59
 Db 1 MAVLALLCLVTFPSQSLQVQLKESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQF 59
 QY 60 PGNKLEWMGYISGITYNPSLKRISITRDTSKNQFFLQNLNVTTGDTSTYYCARSLA 119
 Db 60 PCKGLEWLVITGGVTNYSALKRSLISKNSKQVFLKNSLQTNDRYICARDN 119
 QY 120 RTAMDYWGQGTSTVTVSS 137
 Db 120 YEGAMDYWGQGTSTVTVSS 137

RESULT 3

Q96KX8 PRELIMINARY; PRT; 496 AA.
 AC Q96KX8; 7 LWF-...TAPP-GILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 62
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016369; AAH16369.1; -.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 54.8%; Score 393.5; DB 4; Length 496;

Best Local Similarity 60.0%; Pred. No. 5.3e-32;
 Matches 84; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

QY 7 LWF-...TAPP-GILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 61
 Db 4 LWFLLVAAPRWLVLSQLOESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 63
 QY 62 NKLEWMGYISGITYNPSLKRISITRDTSKNQFFLQNLNVTTGDTSTYYCAR---S 117
 Db 64 KGLEWANTYISGITYNPSLKRISITRDTSKNQFFLQNLNVTTGDTSTYYCARHGYSR 123
 QY 118 LARTAMDYWGQGTSTVTVSS 137
 Db 124 SGRTCAIDYWGQGLTVTVSS 143

RESULT 4

Q96EY0 PRELIMINARY; PRT; 613 AA.
 AC Q96EY0; 7 LWF-...TAPP-GILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 61
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AAH11857.1; -.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 53.8%; Score 386.5; DB 4; Length 613;

Best Local Similarity 61.3%; Pred. No. 3.6e-31;
 Matches 84; Conservative 15; Mismatches 31; Indels 7; Gaps 4;

QY 7 LWF-...TAPP-GILSDVQLQESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 62
 Db 4 LWFLLVAAPRWLVLSQLOESGPNLVKPSQSLTCTVTGYSTSDHAWSWIRQPG 62
 QY 63 KLEWMGYISGITYNPSLKRISITRDTSKNQFFLQNLNVTTGDTSTYYCAR--LAR 120
 Db 63 GLEWIGRIYTSSTNYPNPSLKRISITRDTSKNQFFLQNLNVTTGDTSTYYCAR--LAR 122
 QY 121 TTAMDYWGQGTSTVTVSS 137
 Db 123 TVGLFYWGQGLTVTVSS 139

RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.
 AC Q9UL73
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 53.2%; Score 382; DB 4; Length 119;
Best Local Similarity 66.4%; Pred. No. 1.4e-31;
Matches 79; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 20 VQLQESGPGVLVKPSQSLTCTVTGYGITSDDHAWSWIRQPPGNKLEWNGYISYSGITTYN 79
DB 2 VQLQESGPGVLVKPSETLSLCTVSGSGSICS-YYWSWIRQPPGKLEWIGYIYSGSTNYT 60

QY 80 PSLKSRISITRDTSKNQFFLQNSVTTGDTSTYYCAR-SLARTTAMDYWGQGSTVTVSS 137
DB 61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNWPYYFDYWGQGSTLTVTSS 119

RESULT 6
O95973 ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RA "Clonal proliferation of IgM secreting B cell in the synovium of
RA Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT NON_TER 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 52.1%; Score 374; DB 4; Length 150;
Best Local Similarity 58.8%; Pred. No. 1.1e-30;
Matches 80; Conservative 18; Mismatches 31; Indels 7; Gaps 4;

QY 7 LWLF---TAPP-GILSDVQLQESGPGVLVKPQSLSLTCTVTGYGITS-DHAWSWIRQPPG 61
DB 4 LWFFLLLVAAPRWLSQQLQESGPGVLVKPSETLSLCTVSGSGISSTNYWGIQPPPE 63

QY 62 NLEWNGYISYSGITTYNPSLKSRIITRDTSKNQFFLQNSVTTGDTSTYYCARSLART 121
DB 64 KGLEWIGSLHNSGSDYNNPSLKSRTVISDVTSKNQFSLRLSSVTAAATAVYYCAR--LGM 121

QY 122 TAMDYWGQGSTVTVSS 137
DB 122 GAFDFWGHGTMVTVSS 137

RESULT 7
O9BQ88 ID O9BQ88 PRELIMINARY; PRT; 597 AA.
AC O9BQ88;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR EMBL; BC001872; AAH01872.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 52.1%; Score 374; DB 4; Length 597;
Best Local Similarity 56.3%; Pred. No. 6.7e-30;
Matches 80; Conservative 18; Mismatches 32; Indels 12; Gaps 4;

QY 7 LWLF---TAPP-GILSDVQLQESGPGVLVKPQSLSLTCTVTGYGITS-DHAWSWIRQPPGN 62
DB 4 LWFFLLLVAAPRWLSQQLQESGPGVLVKPSETLSLCTVSGVYGGSF-SGYIWSWIRQPPGK 62

QY 63 KLEWNGYISYSGITTYNPSLKSRIITRDTSKNQFFLQNSVTTGDTSTYYCARSLARTT 122
DB 63 GLEWIGEINHSGITTYNPSLKSRTVISDVTSKQSLKLSLVNAADTAVYYCARVITRAS 122

QY 123 -----AMDYWGQGSTVTVSS 137
DB 123 PGTDGRYGMVDMVGQGTVTVSS 144

RESULT 8
O8WUX4 ID O8WUX4 PRELIMINARY; PRT; 588 AA.
AC O8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019235; AAH19235.1;
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
 Query Match 51.3%; Score 368; DB 4; Length 588;
 Best Local Similarity 55.6%; Pred. No. 2.7e-29;
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;
 QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPNG 62
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGGSF-SGYWWSWIRQPPGK 62
 QY 63 KLEWGVISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSLVTGDTSTYYCARSARTT 122
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDTSKKQLSLKSSVNAADTAVYYCARVITRAS 122
 QY 123 -----AMDYWGQGTSTVTVSS 137
 DB 123 PGTDGRYGMVWVGQGTTVTVSS 144
 RESULT 9
 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
 AC Q9BU10;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AAH02963.1;
 DR HSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
 Query Match 51.3%; Score 368; DB 4; Length 597;
 Best Local Similarity 55.6%; Pred. No. 2.8e-29;
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;

QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPNG 62
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGGSF-SGYWWSWIRQPPGK 62
 QY 63 KLEWGVISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSLVTGDTSTYYCARSARTT 122
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDTSKKQLSLKSSVNAADTAVYYCARVITRAS 122
 QY 123 -----AMDYWGQGTSTVTVSS 137
 DB 123 PGTDGRYGMVWVGQGTTVTVSS 144
 RESULT 9
 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
 AC Q9BU10;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AAH02963.1;
 DR HSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
 Query Match 51.3%; Score 368; DB 4; Length 597;
 Best Local Similarity 55.6%; Pred. No. 2.8e-29;
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;

QY 63 KLEWGVISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSLVTGDTSTYYCARSARTT 122
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDTSKKQLSLKSSVNAADTAVYYCARVITRAS 122
 QY 123 -----AMDYWGQGTSTVTVSS 137
 DB 123 PGTDGRYGMVWVGQGTTVTVSS 144
 RESULT 10
 ID Q96AA6 PRELIMINARY; PRT; 618 AA.
 AC Q96AA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1;
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
 Query Match 51.3%; Score 368; DB 4; Length 618;
 Best Local Similarity 55.6%; Pred. No. 2.9e-29;
 Matches 79; Conservative 18; Mismatches 33; Indels 12; Gaps 4;

QY 7 LWLF---TAFP-GILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQFPNG 62
 DB 4 LWFFLLVAAPRWVLSQVQLQWAGLLKPSLTSLTCGVYGGSF-SGYWWSWIRQPPGK 62
 QY 63 KLEWGVISYSGITTYNPSLKSRIISITRDTSKNQFFLQNSLVTGDTSTYYCARSARTT 122
 DB 63 GLEWIGEINHSGSTNYNPSLKSRTVISDTSKKQLSLKSSVNAADTAVYYCARVITRAS 122
 QY 123 -----AMDYWGQGTSTVTVSS 137
 DB 123 PGTDGRYGMVWVGQGTTVTVSS 144
 RESULT 11
 ID Q99NG4 PRELIMINARY; PRT; 121 AA.
 AC Q99NG4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Single chain Fv (Fragment).
 OS Mus musculus (Mouse).
 OG Plasmid PHEN1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=98169018; PubMed=9510199;
 RA Hawlich H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
 Bautsch W., Kola A., Kios A., Koehl J.;


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RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59DSB CRC64;

Query Match 51.2%; Score 367.5; DB 11; Length 121;
Best Local Similarity 62.5%; Pred. No. 4.5e-30;
Matches 75; Conservative 17; Mismatches 25; Indels 3; Gaps 2;

Qy 20 VQLQESGVLVVKPSQSLTCTVTGYISITSPHAWSWIRQFPGNKLEWNGYISYSGITTYN 79
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 VQLQESGGLVAPQSLSITCTVSGFLTS-HGVSWVRQPPGKGLVGLVIGDGNTRYH 60

Qy 80 PSLKSRISITRDTSKNQFFLOLNSVTTGDTSTYYCARSLAR--TTAMDYWGQGTSTVTVS 137
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 SALISRLSISDKNSQVFLKNSLQTDATYTCARHYKYANYAMDYWGQGTSTVTVS 120

RESULT 12
Q9UL75 PRELIMINARY; PRT; 122 AA.
ID Q9UL75
AC Q9UL75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 50.1%; Score 359.5; DB 4; Length 122;
Best Local Similarity 61.2%; Pred. No. 3e-29;
Matches 74; Conservative 12; Mismatches 32; Indels 3; Gaps 2;

Qy 20 VQLQESGVLVVKPSQSLTCTVTGYISITSPH-AWSWIRQFPGNKLEWNG--YISYSGIT 76
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 VQLQSGGLVAPQSLSITCTVSGFLTS-HGVSWVRQPPGKGLVGLVIGDGNTRYH 61

Qy 77 TYNPSLKRISITRDTSKNQFFLOLNSVTTGDTSTYYCARSLAR--TTAMDYWGQGTSTVTVS 136
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 DYRSVSKSRITNPDTSKNQFSLQNSVTPEDTAVYTCARDLELLIGDPDYGQGTSTVTVS 121

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Qy 137 S 137
Dy 122 S 122

RESULT 13
Q8TC63 PRELIMINARY; PRT; 473 AA.
ID Q8TC63
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 46.9%; Score 336.5; DB 4; Length 473;
Best Local Similarity 51.1%; Pred. No. 3.6e-26;
Matches 69; Conservative 25; Mismatches 36; Indels 5; Gaps 3;

Qy 7 LWLF---TAPP-GILSDVQLQESGVLVVKPSQSLTCTVTGYSI-TSDHAWSWIRQPPG 61
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
11 LWFLLVLAAPRWVLSRLQQLQESGVLVVKPSQSLTCTVTGYSGDVSSVSSYWGVRQPPG 70

Qy 62 NKLEWNGYISYSGITTYNPSLKRISITRDTSKNQFFLOLNSVTTGDTSTYYCARSLAR 121
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 KGLEWIGTINFGNMYSPSLRSRVMTSADMSNSFYKLKLSVTAADTAVYCAAGHLVM 130

Qy 122 TAMDYWGQGTSTVTVS 136
Dy ||||| ||||| |||||
131 GFGAHWGQGLVSVS 145

RESULT 14
Q8IZD7 PRELIMINARY; PRT; 130 AA.
ID Q8IZD7
AC Q8IZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Jang Y.-J., Chung J., Park J.-Y.;
RA "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RA Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -.
FT NON_TER 1 1
FT NON_TER 130 130

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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:14:35 ; Search time 14.5303 Seconds
(without alignments)
398.931 Million cell updates/sec

Title: US-09-114-285A-31

Perfect score: 718

Sequence: 1 MRVLLILWLFTAFPGILSDV.....LARTAMDYWGQGTSTVTSS 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	718	100.0	137	1	US-08-137-117D-31
2	718	100.0	137	2	US-08-436-717-31
3	538	74.9	138	1	US-08-137-117D-69
4	538	74.9	138	2	US-08-436-717-69
5	534	74.4	119	3	US-08-767-128-18
6	534	74.4	130	3	US-08-466-151-5
7	534	74.4	130	4	US-08-466-163B-5
8	527	73.4	123	1	US-08-137-117D-64
9	527	73.4	123	2	US-08-436-717-64
10	518.5	72.2	240	2	US-07-956-399-2
11	500.5	69.7	114	1	US-08-111-080-23
12	500.5	69.7	114	1	US-08-211-980-23
13	500.5	69.7	114	5	PCT-US93-07967-23
14	499	69.5	213	4	US-09-170-769A-2
15	496	69.1	118	3	US-09-065-059-11
16	493	68.7	117	2	US-08-672-345C-13
17	493	68.7	117	3	US-09-214-095D-13
18	491.5	68.5	117	2	US-08-308-494A-13
19	478.5	66.6	241	3	US-08-902-486-13
20	478.5	66.6	496	3	US-08-902-486-15
21	475.5	66.2	638	3	US-09-070-637-20
22	468.5	65.3	137	3	US-08-466-151-7
23	468.5	65.3	137	4	US-08-466-163B-7
24	468	65.2	113	1	US-08-107-669D-5
25	468	65.2	113	1	US-08-472-788A-5
26	468	65.2	113	2	US-08-477-531B-5
27	468	65.2	113	2	US-08-082-842A-5

Sequence 14, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 100, App
Sequence 101, App
Sequence 10, Appl
Sequence 11, Appl
Sequence 102, App
Sequence 106, App
Sequence 119, App
Sequence 12, Appl
Sequence 102, App
Sequence 11, Appl
Sequence 114, App
Sequence 103, App
Sequence 110, App
Sequence 2, Appli
Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-137-117D-31
; Sequence 31, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-31

Query Match      100.0%; Score 718; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVILLWLFTAPPGILSDVQLQESGPVLAVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
DB 1 MRVILLWLFTAPPGILSDVQLQESGPVLAVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
QY 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQGTSTVTSS 137
DB 121 TTAMDYWGQGTSTVTSS 137

RESULT 2
US-08-436-717-31
; Sequence 31, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-31

Query Match      100.0%; Score 718; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVILLWLFTAPPGILSDVQLQESGPVLAVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
DB 1 MRVILLWLFTAPPGILSDVQLQESGPVLAVKPSQSLSLTCTVTGYSITSDHAWSIROPP 60
QY 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
DB 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTAMDYWGQGTSTVTSS 137
DB 121 TTAMDYWGQGTSTVTSS 137

RESULT 3
US-08-137-117D-69
; Sequence 69, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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/
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO internal
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ US-08-767-128-18

Query Match          74.4%; Score 534; DB 3; Length 119;
Best Local Similarity 85.7%; Pred. No. 4.7e-47;
Matches 102; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 19 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDYANNWIRQPPGNKLEWNGYISYSGITSY 60

Qy 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCAMVVA--YAMDYWGQGTSTVTVSS 119

RESULT 6
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185999
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sveboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

us-09-114-285a-31.ra1

Query Match          74.4%; Score 534; DB 3; Length 130;
Best Local Similarity 86.6%; Pred. No. 5.3e-47;
Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 19 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDNANNWIRQPPGNKLEWNGYINHSGITTSY 60

Qy 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCAMVVA--YAMDYWGQGTSTVTVSS 117

RESULT 7
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

us-09-114-285a-31.ra1

Query Match          74.4%; Score 534; DB 4; Length 130;
Best Local Similarity 86.6%; Pred. No. 5.3e-47;
Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 19 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDHAWSWIRQPPGNKLEWNGYISYSGITTY 78
Db 1 DVQLQESGPGVLVKPSQSLTCTVTGYSTSDNANNWIRQPPGNKLEWNGYINHSGITTSY 60

Qy 79 NPSLKSRIISITRDTSKNQFFLQNSVTTGDTSTYTCARSLARTTAMDYWGQGTSTVTVSS 137
Db 61 NPSLKSRIISITRDTSKNQFFLQNSVTTEDTATYTCAMVVA--YAMDYWGQGTSTVTVSS 117

RESULT 8
US-08-137-117D-64
; Sequence 64, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248955 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-2

Query Match 72.2%; Score 518.5; DB 2; Length 240;
Best Local Similarity 82.5%; Pred. No. 4.4e-45;
Matches 99; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 18 SDVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITT 77
Db 122 TVQKLEESGPGVLVKPSQSLTCTVTGYPIITSDYAMDWIRQPPGNKLEWGMGVSYSGSTD 181

QY 78 YNPSLKSRSISITRDTSKNQFFLQNLNSVTTGDTSTYYCARSLARTTTAMDYWGOGTSVTYSS 137
Db 182 YNPSLKSRSISITRDTSKNQFFLQNLNSVTTEDTATYYCARG-GFPYAMDYWGOGTSVTYSS 240

RESULT 11
US-08-111-080-23
; Sequence 23, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629

Query Match 69.7%; Score 500.5; DB 1; Length 114;

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-080-23

Query Match 69.7%; Score 500.5; DB 1; Length 114;
Best Local Similarity 81.5%; Pred. No. 1.1e-43;
Matches 97; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 19 DVQLQESGPGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITY 78
Db 1 EVQLQESGPGVLVKPSQSLTCTVTGYISITSDYAMNIRQPPGNKLEWGMGVIYSYGSTTY 60

QY 79 NPSLKSRSISITRDTSKNQFFLQNLNSVTTGDTSTYYCARSLARTTTAMDYWGOGTSVTYSS 137
Db 61 NPSLKSRSISITRDTSKNLFLLQLSSVTSSTEDTATYYCARG-----SFGDWGOGTLLVTVSA 114

RESULT 12
US-08-211-980-23
; Sequence 23, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-980-23

Query Match 69.7%; Score 500.5; DB 1; Length 114;
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-065-059-11

Query Match 69.1%; Score 496; DB 3; Length 118;
Best Local Similarity 79.7%; Pred. No. 3.4e-43;
Matches 94; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
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Db 1 VOLQESGPVLVKPSQSLTCTVTGYSTSDHAWMIROFPQGNKLEWMGYISYSGITTYN 60
QY 80 PSLKSRISITRDTSKNQFELQNSVTGDTSTYYCARSLARTTANDYWGQTSVTVSS 137
Db 61 PSLKSRISITRDTSKNQFELQNSVTGDTSTYYCARSLARTTANDYWGQTSVTVSS 118

Search completed: October 22, 2003, 22:20:50
Job time : 15.5303 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:16:46 ; Search time 25.428 Seconds
(without alignments)
902.237 Million cell updates/sec

Title: US-09-114-285A-31

Perfect score: 718
Sequence: 1 MRVLILWLFTAFPGILSDVLARTTAMDYWGQTSVTVSS 137

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Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	534	74.4	130	9	US-09-802-077-5 Sequence 5, Appli
2	534	74.4	130	9	US-09-802-096-5 Sequence 5, Appli
3	534	74.4	130	11	US-09-925-179-5 Sequence 5, Appli
4	521	72.6	115	10	US-09-144-886-58 Sequence 58, Appl
5	521	72.6	121	12	US-10-310-674A-36 Sequence 36, Appl
6	518	72.1	115	10	US-09-144-886-59 Sequence 59, Appl
7	512.5	71.4	140	11	US-09-874-141-53 Sequence 53, Appl
8	499.5	69.6	118	15	US-10-184-300A-3 Sequence 3, Appli
9	498	69.4	266	15	US-10-207-655-260 Sequence 260, App
10	498	69.4	550	15	US-10-207-655-270 Sequence 270, App
11	497.5	69.3	136	9	US-09-858-349-2 Sequence 2, Appli
12	494	68.8	119	15	US-10-207-655-258 Sequence 258, App
13	493	68.7	117	11	US-09-940-727B-13 Sequence 13, Appl
14	476.5	66.4	118	15	US-10-184-300A-2 Sequence 2, Appli
15	476.5	66.4	140	11	US-09-874-141-49 Sequence 49, Appl

16	473.5	65.9	118	15	US-10-184-300A-1 Sequence 1, Appli
17	468.5	65.3	121	10	US-09-144-886-70 Sequence 70, Appl
18	468.5	65.3	137	9	US-09-802-077-7 Sequence 7, Appli
19	468.5	65.3	137	9	US-09-802-096-7 Sequence 7, Appli
20	468.5	65.3	137	11	US-09-925-179-7 Sequence 7, Appli
21	462	64.3	117	11	US-09-940-727B-10 Sequence 10, Appl
22	462	64.3	117	11	US-09-940-727B-11 Sequence 11, Appl
23	462	64.3	122	11	US-09-940-727B-102 Sequence 102, App
24	462	64.3	122	11	US-09-940-727B-106 Sequence 106, App
25	459	63.9	280	11	US-09-940-727B-119 Sequence 119, App
26	458.5	63.9	120	11	US-09-874-141-10 Sequence 10, Appl
27	455	63.4	117	11	US-09-940-727B-12 Sequence 12, Appl
28	455	63.4	117	11	US-09-940-727B-114 Sequence 114, App
29	449	62.5	108	11	US-09-940-727B-110 Sequence 110, App
30	449	62.5	121	9	US-09-920-171-2 Sequence 2, Appli
31	449	62.5	121	12	US-10-113-996-2 Sequence 3, Appli
32	449	62.5	134	9	US-09-802-077-3 Sequence 3, Appli
33	449	62.5	134	9	US-09-802-096-3 Sequence 3, Appli
34	449	62.5	134	11	US-09-925-179-3 Sequence 3, Appli
35	428.5	59.7	120	11	US-09-874-141-6 Sequence 6, Appli
36	428.5	59.7	120	12	US-10-171-681-6 Sequence 6, Appli
37	428.5	59.7	120	12	US-10-171-680-6 Sequence 6, Appli
38	426.5	59.4	497	9	US-09-800-729-145 Sequence 145, App
39	422.5	58.8	120	11	US-09-874-141-5 Sequence 5, Appli
40	422.5	58.8	120	12	US-10-171-681-5 Sequence 5, Appli
41	422.5	58.8	120	12	US-10-171-680-5 Sequence 5, Appli
42	421.5	58.7	120	11	US-09-874-141-7 Sequence 7, Appli
43	421.5	58.7	120	12	US-10-171-681-7 Sequence 7, Appli
44	421.5	58.7	120	12	US-10-171-680-7 Sequence 7, Appli
45	419.5	58.4	120	11	US-09-874-141-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Prestia, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Query Match	74.4%	Score 534;	DB 9;	Length 130;
Best Local Similarity	86.6%	Pred. No. 3.8e-43;		
Matches 103;	Conservative	8;	Mismatches	6;
			Indels	2;
			Gaps	1;
Qy	19	DVQLQESGPVLVKPSQSLTCTVTGYSITSDHAWMIROPPGNKLEMMGVISYSGITTY 78		
Db	1	DVQLQESGPVLVKPSQSLTCTVTGYSITSDHAWMIROPPGNKLEMMGVISYSGITTY 60		
Qy	79	NPSLKRSIRISRTDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQTSVTVSS 137		

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 2

US-09-802-096-5

; Sequence 5, Application US/09802096

; Patent No. US20010038839A1

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

; FILE REFERENCE: P0718P2C3US

; CURRENT APPLICATION NUMBER: US/09/802,096

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-802-096-5

Query Match 74.4%; Score 534; DB 9; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 78

Db 1 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 60

QY 79 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 3

US-09-925-179-5

; Sequence 5, Application US/09925179

; Publication No. US20030044858A1

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)

; FILE REFERENCE: P0718P2C1D1C1US

; CURRENT APPLICATION NUMBER: US/09/925,179

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-925-179-5

Query Match 74.4%; Score 534; DB 9; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 78

Db 1 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 60

QY 79 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

Query Match 74.4%; Score 534; DB 11; Length 130;

Best Local Similarity 86.6%; Pred. No. 3.8e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 78

Db 1 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 60

QY 79 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 137

Db 61 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 117

RESULT 4

US-09-144-886-58

; Sequence 58, Application US/09144886

; Patent No. US20020155114A1

; GENERAL INFORMATION:

; APPLICANT: Marks, James D

; APPLICANT: Amersdorfer, Peter

; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize Botulinum Neurotoxins

; FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144,886

; CURRENT FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 115

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone 1

; OTHER INFORMATION: I88 region VH epitope 1

US-09-144-886-58

Query Match 72.6%; Score 521; DB 10; Length 115;

Best Local Similarity 86.6%; Pred. No. 5.7e-42;

Matches 103; Conservative 3; Mismatches 9; Indels 4; Gaps 2;

QY 19 DVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 78

Db 1 EVQLQESGVLVKPSQSLTCTVTGYISITSDHAWSWIRQPPGNKLEWGMGVIYSYGITTY 59

QY 79 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCAWVA--YAMDYWGQGTSTVTSS 137

Db 60 NPSLKSRSITRDTSKNQFFLQNSVTTEDTATYYCARGY---DAMDYWGQGTSTVTSS 115

RESULT 5

US-10-310-674A-36

; Sequence 36, Application US/10310674A

; Publication No. US20030166860A1

; GENERAL INFORMATION:

; APPLICANT: TeGenero GmbH

; TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor

; FILE REFERENCE: 00140/004001

; CURRENT APPLICATION NUMBER: US/10/310,674A

; CURRENT FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 36

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: No. US20030166860A1e1 Sequence

US-10-310-674A-36

Query Match 72.6%; Score 521; DB 12; Length 121;

Best Local Similarity 83.5%; Pred. No. 6e-42;

```
Matches 101; Conservative 6; Mismatches 12; Indels 2; Gaps 1;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLQESGVLVVKPSQSLTCTVTGYSITSDYAWNWIRQPPGNKLEWMGYIRYSGSTY 60
Qy 79 NPSLKSRISTRDTSKNQFFLQLSNVTTGDTSTYYCARSARTT--AMDYWGQGTSTVTS 136
Db 61 NPSLKSRISTRDTSKNQFFLQLSNVTTEDTATYYCARDWPRPSYWFVDMVAGAGTTVTS 120
Qy 137 S 137
Db 121 S 121

RESULT 6
US-09-144-886-59
; Sequence 59, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144.886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 59
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-59

Query Match 72.1%; Score 518; DB 10; Length 115;
Best Local Similarity 86.6%; Pred. No. 1.1e-41;
Matches 103; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 EVQLQESGVLVVKPSQSLTCTVTGYSIT-DYAWNWIRQPPGNKLEWMGYISYSGSTY 59
Qy 79 NPSLKSRISTRDTSKNQFFLQLSNVTTGDTSTYYCARSARTTAMDYWGQGTSTVTS 137
Db 60 NPSLKSRISTRDTSKNQFFLQLSNVTTEDTGTYYCARGY---DAMDYWGQGTSTVTS 115

RESULT 7
US-09-874-141-53
; Sequence 53, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874.141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 53
; LENGTH: 140
; TYPE: PRT
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```
; ORGANISM: Homo sapiens
US-09-874-141-53

Query Match 71.4%; Score 512.5; DB 11; Length 140;
Best Local Similarity 75.5%; Pred. No. 4.5e-41;
Matches 105; Conservative 12; Mismatches 19; Indels 3; Gaps 3;
Qy 1 MRVLILMLFTAPPGILSDVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPP 60
Db 1 MVLISLLYLLTALPGFLSEVQLQESGVLVVKPSQSLTCTVTGDSITNGF-MIWIIRKFP 59
Qy 61 GNKLEWMGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLSNVTTGDTSTYYCA-RSLA 119
Db 60 GNKLEWMGYISYSGITTYNPSLSKRSITRDTSKNQFFLQLSNVTTEDTCTYYCACRSY 119
Qy 120 RTT-AMDYWGQGTSTVTS 137
Db 120 RTPYDFWQGGITLTIVSS 138

RESULT 8
US-10-184-300A-3
; Sequence 3, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184.300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().7)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv7
US-10-184-300A-3

Query Match 69.6%; Score 499.5; DB 15; Length 118;
Best Local Similarity 79.0%; Pred. No. 6.4e-40;
Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
Qy 19 DVQLQESGVLVVKPSQSLTCTVTGYSITSDHAWSWIRQPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLQESGVLVVKPSQSLTCTVTGYSITSDYAWNWIRQPPGNKLEWMGYISYSGTTSY 60
Qy 79 NPSLKSRISTRDTSKNQFFLQLSNVTTGDTSTYYCARSARTTAMDYWGQGTSTVTS 137
Db 61 NPSLKSRISTRDTSKNQFFLQLSNVTTEDTATYYCAREWF-PYYFDYWGQGTTLTVSS 118

RESULT 9
US-10-207-655-260
; Sequence 260, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
```

```
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 260
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-260

Query Match          69.4%; Score 498; DB 15; Length 266;
Best Local Similarity 79.2%; Pred. No. 2.2e-39;
Matches 95; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 18 SDVQLQESGPVLVKPSQSLTCTVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 77
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 146 SDVQLQESGPGLVKPSQSLTCSVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 205
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 78 YNPISLRISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 206 YNPISLRISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 265

RESULT 10
US-10-207-655-270
; Sequence 270, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 270
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-270

Query Match          69.4%; Score 498; DB 15; Length 550;
Best Local Similarity 79.2%; Pred. No. 5.1e-39;
Matches 95; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 18 SDVQLQESGPVLVKPSQSLTCTVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 77
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 146 SDVQLQESGPGLVKPSQSLTCSVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 205
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 78 YNPISLRISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 206 YNPISLRISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 265

RESULT 11
US-09-858-349-2
; Sequence 2, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFVTI peptide
```

```
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (99)..(107)
; OTHER INFORMATION: variable
US-09-858-349-2

Query Match          69.3%; Score 497.5; DB 9; Length 136;
Best Local Similarity 78.3%; Pred. No. 1.2e-39;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 19 DVQLQESGPVLVKPSQSLTCTVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 79 NPSLKSRIISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NPSLKSRIISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 120

RESULT 12
US-10-207-655-258
; Sequence 258, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-258

Query Match          68.8%; Score 494; DB 15; Length 119;
Best Local Similarity 79.0%; Pred. No. 2.1e-39;
Matches 94; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 19 DVQLQESGPVLVKPSQSLTCTVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSDHAWSWIRPPGNKLEWGMGIVSYSGITT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 79 NPSLKSRIISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NPSLKSRIISITRDTSKNQFFLQLNSVTGDTSTYYCARSLARTTAMDYWGQGTSTVTVSS 119

RESULT 13
US-09-940-727B-13
; Sequence 13, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 117
```

```
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-13

Query Match      68.7%; Score 493; DB 11; Length 117;
Best Local Similarity 78.5%; Pred. No. 2.6e-39;
Matches 95; Conservative 8; Mismatches 6; Indels 12; Gaps 2;

Qy 19 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDHAWMIROPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDYANNWIRQPPGNRLEWMGYIRYSGITRY 60

Qy 79 NPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLARTTAMDY-----WGQTSV 133
Db 61 NPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLARTTAMDY-----IHVYGYGNWGQTTIL 113

Qy 134 T 134
Db 114 T 114

RESULT 14
US-10-184-300A-2
; Sequence 2, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Cart, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184.300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv6
US-10-184-300A-2

Query Match      66.4%; Score 476.5; DB 15; Length 118;
Best Local Similarity 76.5%; Pred. No. 9.6e-38;
Matches 91; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

Qy 19 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDHAWMIROPPGNKLEWMGYISYSGITTY 78
Db 1 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDYANNWIRQPPGNKLEWMGYITISY 60

Qy 79 NPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLARTTAMDYWGQTSVTVSS 137
Db 61 NPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLARTTAMDYWGQTSVTVSS 118

RESULT 15
US-09-874-141-49
; Sequence 49, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
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; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; FILE REFERENCE: 037003-Q280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized VH#1 amino acid
US-09-874-141-49

Query Match      66.4%; Score 476.5; DB 11; Length 140;
Best Local Similarity 71.2%; Pred. No. 1.2e-37;
Matches 99; Conservative 14; Mismatches 23; Indels 3; Gaps 3;

Qy 1 MRVLILLWLFAPPGILSDVQLQESGPELVKPSQSLSLTCTVTGYSITSDHAWMIROPP 60
Db 1 MMVLSLLYLLTALPGFLSEVQLQESGPELVKPSQSLSLTCTVTGSDSITNGF-WIWIKPP 59

Qy 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLA 119
Db 60 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQNSVTGDTSTYTCARSLA 119

Qy 120 RTT-AMDYWGQTSVTVSS 137
Db 120 RTPVYDFEWGQTTLTVSS 138

Search completed: October 22, 2003, 22:21:46
Job time : 26.428 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:57:16 ; Search time 976.125 Seconds
(without alignments)
1129.179 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATCAGAGTGTGATCTTTT.....CTCAGTCACCGTCTCTCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281.2	68.4	1420	9	US-09-237-061-2
2	278.6	67.8	363	12	US-10-310-674A-35
3	271.4	66.0	806	14	US-10-207-655-259
4	271.4	66.0	1665	14	US-10-207-655-269
5	269	65.5	354	14	US-10-184-300A-9
6	268	65.2	362	14	US-10-207-655-257
7	260.8	63.5	411	9	US-09-858-349-1
8	259.4	63.1	354	14	US-10-184-300A-8
9	258.2	62.8	366	11	US-09-940-727B-101
10	257.8	62.7	354	14	US-10-184-300A-7
11	255.8	62.2	426	11	US-09-874-141-52
12	255.8	62.2	426	12	US-10-171-681-28
13	255.8	62.2	426	12	US-10-171-680-28
14	253.4	61.7	366	11	US-09-940-727B-105
15	245.6	59.8	420	11	US-09-940-727B-109
16	245.4	59.7	419	11	US-09-940-727B-113
					Sequence 2, Appl
					Sequence 35, Appl
					Sequence 259, App
					Sequence 269, App
					Sequence 9, Appli
					Sequence 257, App
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 101, App
					Sequence 7, Appli
					Sequence 52, Appl
					Sequence 28, Appl
					Sequence 28, Appl
					Sequence 105, App
					Sequence 109, App
					Sequence 113, App

ALIGNMENTS

RESULT 1

US-09-237-061-2
; Sequence 2, Application US/09237061
; Patent No. US20020081624A1
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin
; TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States
; FILE REFERENCE: DM-6956
; CURRENT APPLICATION NUMBER: US/09/237,061
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: 60/072,733
; PRIOR FILING DATE: 1998-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Heavy Chain of
; OTHER INFORMATION: rUK094
US-09-237-061-2

Query Match	68.4%	Score	281.2	DB	9	Length	1420
Best Local Similarity	81.6%	Pred. No.	8e-84				
Mismatches	338	Conservative	0	Mismatches	73	Indels	3
Gaps	1						
Qy	1	ATCAGAGTGTGATCTTTTGTGGCTGTTTCTCAGACCTTTCTGTATCTCTGTCTGTGATGTG	60				
Db	14	ATGAAAGTGTGTGATCTGTGTACCTGTTGACGCCAATCTCTGTATCTCTGTCTGTGATGTA	73				
Qy	61	CAGCTTCAGGAGTCGGACCTGCTCTGGTGAAGCTTCTCAGTCTCTGTCTCTCCCTCACCTGC	120				
Db	74	CAGCTTCAGGAGTCAGACCTGGCTCGTGAACCTTCTCAGTCTCTGTCTCTCACCTGC	133				
Qy	121	ACTGTACTGGCTACTCAATCACAGTGATCATGCCCTGGAGTCGGATCCGCGAGTTTCCA	180				
Db	134	TCTGTACTGGCTACTCCATCACCAGTGGTATTACTTGAACCTGGATCGGCAATTTCCA	193				

Query Match	66.0%; Score 271.4; DB 14; Length 1665;
Best Local Similarity	83.5%; Pred. No. 1.7e-80;
Matches	308; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY	42 TGGTATCCTGTCTGATGTGACGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCCTTC
DB	432 TGGCGGGGATCTGATGTACAGCTTCAGGAGTCAGGACCTGGCTCTGTGAACCTTC
QY	102 GTCTCTGTCCCTCACTCTGCACTGTCACTGGCTACTCAATCAACAGTGATCATGCTCGAG
DB	492 GTCTCTGTCTCACTGCTCTGTGCTACTGGCTACTCCATCAACCAAGTGGTTTCTACTGGAA
QY	162 CTGGATCCGGCAGTTTCAGAGAAACAACCTGGAGTGGTGGCTACATAAAGTTACAGTGG
DB	552 CTGGATCCGACAGTTTCGGGAAACAACTGGAATGGATGGGCGCACATAAGCCACGACGG
QY	222 TATCACTACCTACAAACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAA
DB	612 TAGGAATAACTACAACCCATCTCTCATAAATCGAATCTCCATCACTCGTGACACATCAA
QY	282 GAACCACTTCTCTACAGTTGAATCTGTGACTACTGGGACACAGTCCACATATTCTG
DB	672 GAACCACTTTTCTCTGAAGTTGAGTTCTGTGACTACTGAGGACACAGCTACATATTTCTG
QY	342 TGCAGAGATCCCTAGCTCGGACTACGGCTATGGACTACTCTGGGGTCAAGGAACCTCAGTCAC
DB	732 TGCNAGACACTACGGTAGTCGGGAGCTATGCACTACTGGGGTCAAGGAACCTCAGTCAC
QY	402 CGTCTCCTC 410
DB	792 CGTCTCCTC 800

RESULT 5

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US-10-184-300A-9
; Sequence 9, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184,300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..(?)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHV7
US-10-184-300A-9

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7. RESULT

US-09-858-349-1
; Sequence 1, Application US/09858349
; Patent No. US20020012909A1

Db	61	ACCTGCACCTGCTACTCAATCACACAGTGAATTATGCTCTGGAACTGGATACGGCAG	120
Qy	175	TTTTCCAGGAAACAAACTGGAGTGGGCTACATAAAGTTTACAGTGGGTATCACTACCTAC	234
Db	121	TTTTCCAGGAAACAAACTGGAGTGGGCTACATAAACCCTACAGTGGTACCACTAGCTAC	180
Qy	235	AACCCATCTCTCAAAAGTCGAATCTTATCAGTTCGAGACACATCCAAAGAACCAAGTTCTTC	294
Db	181	AACCCATCTCTCAAAAGTCGAATCTTATCTCTCGGACACATCCAAAGAACCAAGTTCTTC	240
Qy	295	CTACAGTTGAATCTCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCCCTA	354
Db	241	CTGAGTTGAATCTCTGTGACTCTTGAGACACAGCCACATATTACTGTGCAAGAGATGG	300
Qy	355	GCTCGGCATACGGCTATGGACTACTGGGGTCAAGGAACTCAGTCACCGTCTCTCTCA	411
Db	301	TTTC--CTTACTATTGACTACTGGGGCAAGGCCACTCTCACAGTCTCTTCA	354

RESULT 6
 US-10-207-655-257
 ; Sequence 257, Application US/10207655
 ; Publication No. US20030118592A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; CURRENT FILING DATE: 2002-07-25
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 257
 ; LENGTH: 362
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion polynucleotide
 US-10-207-655-257

Db	61	ACCTGCACCTGCTACTCAATCACACAGTGAATTATGCTCTGGAACTGGATACGGCAG	120
Qy	175	TTTTCCAGGAAACAAACTGGAGTGGGCTACATAAAGTTTACAGTGGGTATCACTACCTAC	234
Db	121	TTTTCCAGGAAACAAACTGGAGTGGGCTACATAAACCCTACAGTGGTACCACTAGCTAC	180
Qy	235	AACCCATCTCTCAAAAGTCGAATCTTATCAGTTCGAGACACATCCAAAGAACCAAGTTCTTC	294
Db	181	AACCCATCTCTCAAAAGTCGAATCTTATCTCTCGGACACATCCAAAGAACCAAGTTCTTC	240
Qy	295	CTACAGTTGAATCTCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCCCTA	354
Db	241	CTGAGTTGAATCTCTGTGACTCTTGAGACACAGCCACATATTACTGTGCAAGAGATGG	300
Qy	355	GCTCGGCATACGGCTATGGACTACTGGGGTCAAGGAACTCAGTCACCGTCTCTCTCA	411
Db	301	TTTC--CTTACTATTGACTACTGGGGCAAGGCCACTCTCACAGTCTCTTCA	354

RESULT 6

US-10-207-655-257

; Sequence 257, Application US/10207655

; Publication No. US20030118592A1

; GENERAL INFORMATION:

; APPLICANT: Ledbetter, Jeffrey A.

; APPLICANT: Hayden-Ledbetter, Martha S.

; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

; FILE REFERENCE: 390069.401C1

; CURRENT APPLICATION NUMBER: US/10/207,655

; CURRENT FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 426

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 257

; LENGTH: 362

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: fusion polynucleotide

US-10-207-655-257

7. RESULT

US-09-858-349-1
; Sequence 1, Application US/09858349
; Patent No. US20020012909A1

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; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 411
; TYPE: DNA
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFVFI peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (295)..(320)
; OTHER INFORMATION: a or g or c or t/u
US-09-858-349-1

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Query Match	63.5%	Score 250.8	DB 9	Length 411	
Best Local Similarity	82.3%	Prod. No. 3.4e-77			
Matches 293	Conservative	6	Mismatches 54	Indels 3	Gaps 1
Qy	55	GATGTGCAGCTTCAGGAGTCGGGACCTCTCCTGGTGAAGCCTTCTCAGTCTCTGTGTCCTC	114		
Db	1	GATGTGCAGCTGCAGGAGTCAGGACCTGGCTCGTGAACCTTCTCAGTCTCTGTGTCCTC	60		
Qy	115	ACCTGCACCTGTCACTGGCTACTCAATCACCACTGATCATGCTCGAGCTGGATCGGCAG	174		
Db	61	ACCTGCTCTGCACTGGCTACTCATCACCACTGGTTATTACTGGAATCGATCGGCAG	120		
Qy	175	TTTCCAGGAAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCACTACCTAC	234		
Db	121	TTTCCAGGAAACAACTGGAATGGATGGCTACATAAGCTACGATGGTAGCAATAACTAC	180		
Qy	235	AACCCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACAGTTCTTC	294		
Db	181	AACCCATCTCTCAAATAATCGAATCTCCATCACTCGTGACACATCTAAGAACCAAGTTTTC	240		
Qy	295	CTACAGTTGAATTTCTGTGACTACTGGGGACACGCTCCACATATTACTGTGCAAGA---TCC	351		
Db	241	CTGAAGTTGAATTTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGANNKNNK	300		
Qy	352	CTAGCTCGGACCTACGGCTATGGACTACTGGGGTCAAGAACTCAGTCACCGTCTC	407		
Db	301	NNKNNKNNKNNKNNKNNKNNKGACTACTGGGGCCAAAGGGAACACTGTCAACCGTCGC	356		

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RESULT 8
US-10-184-300A-8
; Sequence 8, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184.300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

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; OTHER INFORMATION: Synthetic construct of 3B6DIVHV6
US-10-184-300A-8

Query Match          63.1%; Score 259.4; DB 14; Length 354;
Best Local Similarity 84.9%; Pred. No. 9.3e-77;
Matches 303; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTGCCCTC 114
Db 1 GATGTGCAGCTTAAAGAGTCGGGACCTGGGCTGGTTAAACCTACTCAGACTCTGCACCTC 60

Qy 115 ACCTGCACCTGCTACTGGCTACTCAATACACAGTGATCATGCCTGGAGCTGGATCCGGCAG 174
Db 61 ACCTGCACCTGCTACTGGCTACTCAATACACAGTGATTCGCCTGGAACTGGATACGGCAG 120

Qy 175 TTTTCCAGGAACAAACCTGGAGTCGGTGGGCTACATAAGTTACAGTCGGTATCACTACCTAC 234
Db 121 CCACCCAGGAAGGGACTGGAGTCGGTGGGCTACATAACCTACAGTCGGTACCATAGCTAC 180

Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTCTTTC 294
Db 181 AACCCATCTCTCAAGTCGAATCTCTATCTCTCGGCACACATCCAAAGAACCAAGTCTTTC 240

Qy 295 CTACAGTTGAATTTCTGTGACTACTGGGGACACGCTCCACATATTTACTGTGCAAGATCCCTA 354
Db 241 CTGCAGTTGAATTTCTGTGACTTCTGAGGACACAGCCACATATTTACTGTGCAAGAGAGTG 300

Qy 355 GCTCGGACTACGGCTATGGACTACTGGGTCAAGGAACCTCAGTCAACCGTCTCCTCA 411
Db 301 TTTTCTCTTACTACTTGTGACTACTGGGGCAAGGCACCACTCTCAGTCTCTTCA 354

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RESULT 9
US-09-940-727B-101
; Sequence 101, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04, 095
; PRIOR APPLICATION NUMBER: 09/214, 095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 366
; TYPE: DNA
; ORGANISM: mouse
; US-09-940-727B-101

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	Query Match	62.8%;	Score 258.2;	DB 11;	Length 366;
	Best Local Similarity	84.9%;	Pred. No. 2.4e-76;		
	Matches 303;	Conservative	0;	Mismatches 48;	Indels 6; Gaps 1;
QY	55	GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTTCTCAGTCTCTGTGCCCTC	114		
DB	1	GATGTGCAGCTTCAGGAGTCGGGACCTGGCGCTGGTGAACCTTCTCAGTCTCTGTGCCCTC	60		
QY	115	ACCTGCACCTGTCACTGGCTACTCAATCACCAAGTGATCGCTCGGAGCTGGATCCGGCAG	174		
DB	61	ACCTGCACCTGTCACTGGCAATTCAATCACCAAGTGATTTATGCCCTGGACCTGGATCCGGCAG	120		
QY	175	TTTTCAGGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTAC	234		
DB	121	TTTTCAGGAAACAAACTGGAGTGGATGGGCTACATAAGGCACATTTATGGCATTAGGTAC	180		
QY	235	AAACCCATCTCTCAAAAGTCGAATCTCTATCACTTCGAGACACATCCCAAGAACCAAGTTCTTC	294		

Db 181 AACCTTCTCTCATAAGTCGAATCTCTATCATCTCGAGACAGCTCCAAAGAACCAAGTTCTTC 240
Qy 295 CTACAGTTGAATTCCTGACTACTGGGACACGTCACATATTAAGTGGCAAGATCCCTA 354
Db 241 CTGAGTTGGATTCTGACTGCTGAGGACACAGCCACATATTAATGTTGAAGATATCAT 300
Qy 355 GCTCGACTACGGCTATGACTACTGCGGTCAAGAAACCTCAGTCACCGTCTCCTCA 411
Db 301 TACTACGGTTCGGCT-----TACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351

RESULT 10
US-10-184-300A-7
; Sequence 7, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
; APPLICANT: Cart, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: Carrier molecules
; FILE REFERENCE: 229752001700
; CURRENT APPLICATION NUMBER: US/10/184.300A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00827
; PRIOR FILING DATE: 2002-10-26
; PRIOR APPLICATION NUMBER: US 60/301,154
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/300,947
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Synthetic construct of 3B6DIVHv5
US-10-184-300A-7

Query Match 62.7%; Score 257.8; DB 14; Length 354;
Best Local Similarity 84.6%; Pred. No. 3.2e-76;
Matches 302; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

Qy 55 GATGTCAGCTTCAGGAGTCGGACCTCTCTGTTGAAGCCTTCTCAGTCTCTGTCCCTC 114
Db 1 GATGTCAGCTTAAGGAGTCGGACCTGGCTTGGTTAAACCTTACTCAGACTCTGACCCCTC 60
Qy 115 ACCTGCACTGCTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAG 174
Db 61 ACCTGCACTGCTCAGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAG 120
Qy 175 TTTCAGGAACAAACTCGAGTGGATGGGTACATAAGTTACAGTGGTATCAGTACCTAC 234
Db 121 CCACAGGAAGGAGTCTGAGTGGATGGGTACATAAACCTACAGTGGTACCAGTACTAC 180
Qy 235 AACCCATCTCTCAAAGTCGAATCTCTATCATCTCGAGACATCCAGAACCAAGTCTTTC 294
Db 181 AACCCATCTCTCAAAGTCGAATCTCTATCTCTCGGACACATCCAGAACCAAGTCTTTC 240
Qy 295 CTACAGTTGAATTCCTGACTACTGGGACACGTCACATATTAAGTGGCAAGATCCCTA 354
Db 241 CTGAGTTGAATTCCTGACTCTGAGGACACAGCCACATATTAAGTGGCAAGAGAGTGG 300
Qy 355 GCTCGACTACGGCTATGACTACTGCGGTCAAGAAACCTCAGTCACCGTCTCCTCA 411
Db 301 TTTC---CTTACTACTTTGACTACTGGGGCCAAAGGACCACCTCTCAGAGTCTCTTCA 354

RESULT 11
US-09-874-141-52
; Sequence 52, Application US/09874141

; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(426)
US-09-874-141-52

Query Match 62.2%; Score 255.8; DB 11; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.6e-75;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

Qy 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTACAGCCCTTCTGTGATCTCTGTCTGATGTG 60
Db 7 ATGATGGTGTAAAGTCTTCTGTACTCTTGACAGCCCTTCCGGGTTTCTGTGTACAGAGTG 66
Qy 61 CAGCTTCAGGAGTCGGACCTGCTGTTGAAGCCTTCTCAGTCTCTGCTCCCTCACCTGC 120
Db 67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAACCTTCTCAGACTCTGTCCCTCACCTGT 126
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGCGCAGTTTCCA 180
Db 127 TCTGTCACTGGGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAATTTCCA 183
Qy 181 GGAACAACTGGAGTGGATGGGTACATAGTTACAGTGGTATCAGTACTACCAACCCA 240
Db 184 GGAATAAATCTGAGTACATGGGTACATAAGTTACAGTGGTAGCACTTACTACAATCCA 243
Qy 241 TCTCTCAAAGTCAATCTCTATCAGTCGACACATCCAGAACCAAGTCTTCTCTACAG 300
Db 244 TCTCTCAAAGTCAATCTCTATCAGTCGACACATCCAGAACCAAGTCTTCTCTACAA 303
Qy 301 TTGAATTCGTGACTACTGGGGACACGTCACATATTAAGTGTGCAAGATCCCTAGCTCGG 360
Db 304 TTGAATTCGTGACTACTGAGGACACAGGCACATATTAAGTGTGCTGCTGCGGAGTTACGGG 363
Qy 361 ACTACGGC-----TATGACTACTGGGGTCAAGAAACCTCAGTCACCGTCTCCTCA 411
Db 364 AGGACCCCGTACTACTTTGACTTCTGGGGCCAAAGGACCACCTCTCAGCGTCTCCTCA 420

RESULT 12
US-10-171-681-28
; Sequence 28, Application US/10171681
; Publication No. US20030170233A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404

```

; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/171,681
; FILING DATE: 17-JUNE-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..426
; US-10-171-681-28

Query Match 62.2%; Score 255.8; DB 12; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.6e-75;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

QY 1 ATGAGAGTCTGATCTTTTGGTGTTCACAGCCTTTCCTGGTATCTCTGTCTGATGTG 60
DB |||||
7 ATGATGGTGTAAAGTCTTCTGTACCTGTGACAGCCCTTCCGGGTTTCTCTGTCAGAGGTG 66
QY 61 CAGCTTCAGGAGTCGGGACCTGCTCGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB |||||
67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAAGCCTTCTCAGACTCTGTCCCTCACCTGT 126
QY 121 ACTGTCTAGTCTACTCAATCACCAGTGATCATCGCTGGAGCTGGATCCGGCAGTTTCCA 180
DB |||||
127 TCTGTCACTGGGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAAATTTCCA 183
QY 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGTGTATCTACTACCAACCCA 240
DB |||||
184 GGAATAACTTGAGTACATGGGTACATAAGTTACAGTGTGTAGTCTACTACAATCCA 243
QY 241 TCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCCAAGACCATCTTCTCTACAG 300
DB |||||
244 TCTCTCAAGAGTCGAATCTCTCACTCGCGACACATCCCAAGACCATCTTCTACCTACAA 303
QY 301 TTGAATTCGTGACTACTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTGG 360
DB |||||
304 TTGAATTCGTGACTACTGAGACACAGGCACATATTACTGTGCGCCGCGAGTTACGGG 363
QY 361 ACTACGGC-----TATGACTACTTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCA 411
DB |||||
364 AGGACCCCTACTACTTTTGTGCTTCTGGGGCCCAAGGCACCACTCTCAGCGGTCTCTCA 420

RESULT 13
US-10-171-680-28
; Sequence 28, Application US/10171680
; Publication No. US20030175269A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/171,680
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/332,595
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..426
; US-10-171-680-28

Query Match 62.2%; Score 255.8; DB 12; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.6e-75;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

QY 1 ATGAGAGTCTGATCTTTTGGTGTTCACAGCCTTTCCTGGTATCTCTGTCTGATGTG 60
DB |||||
7 ATGATGGTGTAAAGTCTTCTGTACCTGTGACAGCCCTTCCGGGTTTCTCTGTCAGAGGTG 66
QY 61 CAGCTTCAGGAGTCGGGACCTGCTCGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB |||||
67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAAGCCTTCTCAGACTCTGTCCCTCACCTGT 126
QY 121 ACTGTCTAGTCTACTCAATCACCAGTGATCATCGCTGGAGCTGGATCCGGCAGTTTCCA 180
DB |||||
127 TCTGTCACTGGGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAAATTTCCA 183
QY 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGTGTATCTACTACCAACCCA 240
DB |||||
184 GGAATAACTTGAGTACATGGGTACATAAGTTACAGTGTGTAGTCTACTACAATCCA 243
QY 241 TCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCCAAGACCATCTTCTCTACAG 300
DB |||||
244 TCTCTCAAGAGTCGAATCTCTCACTCGCGACACATCCCAAGACCATCTTCTACCTACAA 303
QY 301 TTGAATTCGTGACTACTGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTGG 360
DB |||||
304 TTGAATTCGTGACTACTGAGACACAGGCACATATTACTGTGCGCCGCGAGTTACGGG 363
QY 361 ACTACGGC-----TATGACTACTTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCA 411
DB |||||
364 AGGACCCCTACTACTTTTGTGCTTCTGGGGCCCAAGGCACCACTCTCAGCGGTCTCTCA 420
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[illegible]

RESULT 14

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US-09-940-727B-105
; Sequence 105, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 366
; TYPE: DNA
; ORGANISM: mouse
US-09-940-727B-105

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Query Match 61.7%; Score 253.4; DB 11; Length 366;
Best Local Similarity 84.0%; Pred. NO. 9.8e-75;
Matches 300; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

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Db	1	GACGTGCAGTTGCAGGAGTCGGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCCTC	60
Qy	115	ACCTGCACCTGTCACTGGCTACTCAATCACCAGTGATCATGCTCGAGCTGGATCGGCAG	174
Db	61	ACCTGCACCTGTCACTGGCAATTCAATCACCAGTGATTATGCTCGACCTGGATCGGCAG	120
Qy	175	TTTTCAGGAAACAACTCGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTAC	234
Db	121	TTTTCAGGAAACAACTCGAGTGGATGGCTACATAAAGGCATTTATGGCACTAGGTAC	180
Qy	235	AACCCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACAGTTCTTC	294
Db	181	AACCCCTTCTCATTAAGTCGAACTCTATCACTCGAGACACGTCCAAGAACAGTTCTTC	240
Qy	295	CTACAGTTGAAATTCGTGACTACTCGGGACACGTCACATATTTACTGTGCAAGATCCCTA	354
Db	241	CTGCAGTTGGATTCTGTGACTCTGAGGACACAGCCACATATTTATGTGAAGATATCAT	300
Qy	355	GCTCGGACTACGGCTATGCACTACTGGGTCAAGGAACTCAGTACCCTGTCTCTCA	411
Db	301	TACTACGGTTCGGCT-----TACTGGGSCCAAGGACTCTGGTCACTGTCTCTGCA	351

RESULT 15

US-09-940-727B-109
; Sequence 109, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095

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; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 109
; LENGTH: 420
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: any nucleotide
; US-09-940-727B-109

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Query Match	59.8%;	Score 245.6;	DB 11;	Length 420;
Best Local Similarity	87.4%;	Pred. No. 4.3e-72;		
Matches 292; Conservative	0;	Mismatches 36;	Indels 6;	Gaps 2;

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Qy	130	GGCTACTCAATACCAGTGATCATGCTCGGAGCTGGATCCGGCAGTTCCTCAGGAAACAA	189
Db	107	GGCTACTCAATACCAGTGATTCGCTCGGAACCTGGATCCGGCAGTTCCTCAGGAAACAGA	166
Qy	190	CTGGAGTGGATGGCTACATAAGTTACAGTGGTATCACTCCTACAAACCCTCTCTCAAA	249
Db	167	CTGGAGTGGATGGGCTACATAAGGTACAGTGGTATCACTAGGTACAAACCCTCTCTCAAA	226
Qy	250	AGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTCCTACAGTTGAATCT	309
Db	227	AGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTCCTCAGTTAAATCT	286
Qy	310	GTGACTACTGGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCTCGGACTACGGCT	369
Db	287	GTGACTACTGAGGACACAGCCACTTATTACTGTGTAAGA-----ATTCAATTACTACGGCT	341
Qy	370	ATGGACTACTGGGGTCAAGGAACCTCAGTCAACG	403
Db	342	ACGG-CAACTGGGGGCAAGGCACCACTCTCAAG	374

Search completed: October 24, 2003, 06:22:18
Job time : 977.625 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:51:21 ; Search time 58.1212 Seconds
(without alignments)
3121.209 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATGAGAGTGTGATTCTTTT.....CCTCAGTCACCGTCTCCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	1	US-08-137-117D-30
2	411	100.0	411	1	US-08-436-717-30
3	297.8	72.5	357	3	US-08-767-128-17
4	284.6	69.2	836	2	US-08-933-616-1
5	284.6	69.2	836	3	US-08-279-307-1
6	284.6	69.2	836	4	US-09-135-121B-3
7	277.6	67.5	720	2	US-07-956-399-1
8	264.4	64.3	354	3	US-09-065-059-12
9	260	63.3	639	4	US-09-170-769A-1
10	258.2	62.8	366	2	US-08-672-345C-87
11	258.2	62.8	366	3	US-09-214-095D-101
12	255.8	62.2	426	3	US-08-554-840-28
13	255.8	62.2	426	4	US-08-925-339-28
14	255.8	62.2	426	4	US-09-332-595-28
15	253.4	61.7	366	2	US-08-672-345C-89
16	253.4	61.7	366	3	US-09-214-095D-105
17	250.2	60.9	351	2	US-08-308-494A-14
18	245.6	59.8	420	3	US-09-214-095D-109
19	245.4	59.7	419	3	US-09-214-095D-113
20	244	59.4	830	1	US-08-133-011-115
21	244	59.4	830	1	US-08-322-730A-115
22	244	59.4	830	1	US-08-387-874-88
23	244	59.4	830	2	US-08-383-619-115
24	244	59.4	830	3	US-08-907-739-115
25	244	59.4	830	4	US-09-729-597-115
26	244	59.4	830	5	PCT-US93-08364-88
27	243.4	59.2	2010	3	US-09-070-637-19

ALIGNMENTS

RESULT 1

US-08-137-117D-30

; Sequence 30, Application US/08137117D

; Patent No. 5795965

; GENERAL INFORMATION:

; APPLICANT: TSUCHIYA, Masayuki

; APPLICANT: SATO, Koh

; APPLICANT: BENDIG, Mary

; APPLICANT: JONES, Steven

; APPLICANT: SALDANHA, Jose

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

; NUMBER OF SEQUENCES: 158

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/137,117D

; FILING DATE: 20-DEC-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 4-32084

; FILING DATE: 19-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 3-95476

; FILING DATE: 25-APR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 53466/126/AAOK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 411 base pairs

; TYPE: nucleic acid

Sequence 99, Appl
Sequence 99, Appl
Sequence 71, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 71, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 3, Appl
Sequence 62, Appl
Sequence 1, Appl

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/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..411
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 1..411
US-08-137-117D-30

Query Match 100.0%; Score 411; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.6e-132;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTCTGATCTTTTGGGTGTTTCACAGCCTTTCCTGGTATCCTGTCGTGATGTG 60
Db 1 ATGAGAGTCTGATCTTTTGGGTGTTTCACAGCCTTTCCTGGTATCCTGTCGTGATGTG 60

QY 61 CAGCTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 61 CAGCTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120

QY 121 ACTGTCAGTGGTACTCAATCAACAGTATGATGCTGAGTGGATCGGCGAGTTTCCA 180
Db 121 ACTGTCAGTGGTACTCAATCAACAGTATGATGCTGAGTGGATCGGCGAGTTTCCA 180

QY 181 GGAACAACTGAGTGGATGGGTACATAAGTTACAGTGGTATCAGTACCTACCAACCCA 240
Db 181 GGAACAACTGAGTGGATGGGTACATAAGTTACAGTGGTATCAGTACCTACCAACCCA 240

QY 241 TCTCTCAAAGTCGAATCTCTATCAGTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 300
Db 241 TCTCTCAAAGTCGAATCTCTATCAGTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 300

QY 301 TTGAATTTCTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 301 TTGAATTTCTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGG 360

QY 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
Db 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411

RESULT 3
US-08-436-717-30
; Sequence 30, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/436,717
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
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APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...357
OTHER INFORMATION:
US-08-767-128-17

Query Match 72.5%; Score 297.8; DB 3; Length 357;
Best Local Similarity 89.6%; Pred. No. 5.6e-93;
Matches 320; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 55 GATGTGACGTTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGCTCCCTC 114
Db 1 GATGTGACGTTTCAGGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGCTCCCTC 60
Qy 115 ACCTGCACTGTCAGTGGTCTACTCAATCACCAGTGCATGCTGGAGCTGGATCGGCGAG 174
Db 61 ACCTGCACTGTCAGTGGTCTACTCAATCACCAGTGCATGCTGGAGCTGGATCGGCGAG 120
Qy 175 TTTCAGGAAACAACTCGAGTGGATGGGTACATAAGTTACAGTGGTATCAGTCTACCTAC 234
Db 121 TTTCAGGAAACAACTCGAGTGGATGGGTACATAAGTACAGTGGTATCAGTCTACCTAC 180

Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCAAGTCTTTC 294
Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCCAAGAACCAAGTCTTTC 240
Qy 295 CTACAGTTGAATCTGTGACTACTGGGACACGCTCCACATATTACTGTGCAAGATCCCTA 354
Db 241 CTGAGTTGAATCTGTGACTACTGGGACACGCTCCACATATTACTGTGCAAGATGGGT 300
Qy 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 301 AACTACCCGTGGTACTTTGACTACTGGGGCAAGGACCACTCTCACAGTCTCTCTCA 357

RESULT 4

US-08-933-616-1
Sequence 1, Application US/08933616
Patent No. 5869331
GENERAL INFORMATION:
APPLICANT: Dornburg, Ralph C.
TITLE OF INVENTION: Cell-Type Specific Gene Transfer Using
Retroviral Vectors Containing Antibody-Envelope Fusion
PROTEINS AND WILD-TYPE ENVELOPE FUSION PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P. O. Box 1267
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08551
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/205,980
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-025
TELEPHONE: (609) 466-3407
TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-933-616-1

Query Match 69.2%; Score 284.6; DB 2; Length 836;
Best Local Similarity 84.2%; Pred. No. 3.1e-88;
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;
Qy 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTACAGCCCTTCTGATCTCTGATGTG 60
Db 43 ATGAGTGTGTAAGTCTTCTGTACCTTGTGACAGCCCTTCCGGGTATCTGTGAGAGTG 102
Qy 61 CAGCTTCAGGAGTCGGGACCTGCTGTAAGCCTTCTCAGTCTCTGCTCCCTCACCTGC 120
Db 103 CAGCTTCAGGAGTCAGGACCTAGCCTGTGAAACCTTCTGTGACTCTGTCTCTCACCTGT 162
Qy 121 ACTGTCACTGGTACTCAATCACCAGTGCATGCTCTGGAGCTGGATCCGSCAGTTTCCA 180

Db 163 TCTGTCACTGGGACTCCATCACCAGTGTTA---CTGGAACCTGGATCCGGAATATCCCA 219
Qy 181 GGAACAACTGAGTGGGATGGCTACATAAGTTACAGTGGTATCACTACCTACCAACCA 240
Db 220 GGAATAAACTTGGTACATGGGTACATAAAGTACAGTGGTAGCATTACTACCAATCCA 279
Qy 241 TCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACGAGTTCTTCTACAG 300
Db 280 TCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACGAGTTACTACCTGCAG 339
Qy 301 TTGAATTTGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 340 TTGAATTTGTGACTACTGGGACACAGCCACATATTACTGTGCAAGAT---ATGGTGGT 396
Qy 361 ACTACGGCTATGACTACTGGGGTCAAGAACTCAGTCACCGTCTCCTCA 411
Db 397 AACTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 447

RESULT 5
US-08-279-307-1
; Sequence 1, Application US/08279307
; Patent No. 6146885
; GENERAL INFORMATION:
; APPLICANT: Dornburg, Ralph C.
; TITLE OF INVENTION: Cell-Type Specific Gene Transfer
; TITLE OF INVENTION: Using Retroviral Vectors Containing Antibody-Envelope
; TITLE OF INVENTION: Fusion Proteins
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,307
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,619
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UM01-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 836 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-279-307-1

Query Match 69.2%; Score 284.6; DB 3; Length 836;
Best Local Similarity 84.2%; Pred. No. 3.1e-88;
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;
Qy 1 ATGAGAGTCTGATCTTTTGTGGCTGTTACAGCCTTTCCTGGTATCTCTGCTGATGTG 60
Db 43 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCCGGGTATCTCTGTAGAGGTG 102

Qy 61 CAGCTTCAGGAGTCGGACCTGTCTGTGTAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 103 CAGCTTCAGGAGTCAGGACCTAGCTCGTGAACCTTCTCTGACTCTGTCCCTCACCTGT 162
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGAGTTTCCA 180
Db 163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACCTGGATCCGGAATATCCCA 219
Qy 181 GGAACAACTGAGTGGGTGATAGTTACAGTGGTATCACTACCTACCAACCA 240
Db 220 GGAATAAACTTGGTACATGGGTACATAAGTACAGTGGTAGCATTACTACCAATCCA 279
Qy 241 TCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACGAGTTCTTCTACAG 300
Db 280 TCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACGAGTTACTACTGCGAG 339
Qy 301 TTGAATTTGTGACTACTGGGACACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 340 TTGAATTTGTGACTACTGGGACACAGCCACATATTACTGTGCAAGAT---ATGGTGGT 396
Qy 361 ACTACGGCTATGACTACTGGGGTCAAGAACTCAGTCACCGTCTCCTCA 411
Db 397 AACTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 447

RESULT 6
US-09-135-121B-3
; Sequence 3, Application US/09135121B
; Patent No. 6534051
; GENERAL INFORMATION:
; APPLICANT: Dornburg, Ralph C.
; TITLE OF INVENTION: CELL TYPE SPECIFIC GENE TRANSFER USING RETROVIRAL VECTORS
; TITLE OF INVENTION: CONTAINING ANTIBODY-ENVELOPE FUSION PROTEINS AND WILD-TYPE
; FILE REFERENCE: 97,216-L
; CURRENT APPLICATION NUMBER: US/09/135,121B
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: US 08/933,616
; PRIOR FILING DATE: 1997-08-28
; PRIOR APPLICATION NUMBER: US 08/205,980
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 07/979,619
; PRIOR FILING DATE: 1992-11-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: B6.2 gene encoding single chain antibody against hapten DNP
US-09-135-121B-3

Query Match 69.2%; Score 284.6; DB 4; Length 836;
Best Local Similarity 84.2%; Pred. No. 3.1e-88;
Matches 346; Conservative 0; Mismatches 59; Indels 6; Gaps 2;
Qy 1 ATGAGAGTCTGATCTTTTGTGGCTGTTACAGCCTTTCCTGGTATCTCTGCTGATGTG 60
Db 43 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCCGGGTATCTCTGTAGAGGTG 102
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGTGTAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 103 CAGCTTCAGGAGTCAGGACCTAGCTCGTGAACCTTCTCTGACTCTGTCCCTCACCTGT 162
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGAGTTTCCA 180
Db 163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACCTGGATCCGGAATATCCCA 219
Qy 181 GGAACAACTGAGTGGGTGATAGTTACAGTGGTATCACTACCTACCAACCA 240
Db 220 GGAATAAACTTGGTACATGGGTACATAAGTACAGTGGTAGCATTACTACCAATCCA 279

Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTCTTCTCTACAG 300
Db 280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAAGAACCAAGTCTCTCTGAG 339
Qy 301 TTGAATCTGTGACTACTGGGACACGTCACATATCTGTGCAAGATCCCTAGCTCGG 360
Db 340 TTGAATCTGTGACTACTGGGACACGTCACATATCTGTGCAAGAT---ATGGTGGT 396
Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 447

RESULT 7

US-07-956-399-1
; Sequence 1, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956.399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
US-07-956-399-1

Query Match 67.5%; Score 277.6; DB 2; Length 720;
Best Local Similarity 88.2%; Pred. No. 7.4e-86;
Matches 314; Conservative 0; Mismatches 39; Indels 3; Gaps 1;
Qy 56 ATGTGACGCTTCAGGAGTCGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCA 115
Db 368 AGGTCAAACTCGAGGAGTCGGACCTGGCGCTGGTGAACCTTCTCAGTCTCTGTCCTCA 427
Qy 116 CTGACGCTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGAGTCGGGAGT 175
Db 428 CTGACGCTGTCACTGGCTACCCAAATCACCAGTGATTTATGCTGGAGCTGGAGTCGGGAGT 487

Qy 176 TTCAGAAACAACTGGAGTGGCTTACATAAGTTACAGTGGTATCACTACCTACA 235
Db 488 TTCAGAAACAACTGGAGTGGCTTACATAAGTTACAGTGGTATCACTACCTACA 547
Qy 236 ACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTCTTCTCC 295
Db 548 ACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTCTTCTCC 607
Qy 296 TACAGTTGAATTTCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATCCCTAG 355
Db 608 TGCAGTTGAATTTCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATCCCTAG 664
Qy 356 CTCGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 665 GTTCCCTATGCTATGGACTACTGGGGTCAAGGGACCGGTCACTCTCTCTCA 720

RESULT 8

US-09-065-059-12
; Sequence 12, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAYAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: 50356-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
US-09-065-059-12

Query Match 64.3%; Score 264.4; DB 3; Length 354;
Best Local Similarity 84.2%; Pred. No. 1.8e-81;
Matches 298; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Qy 58 GTGAGCTTCAGGAGTCGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACC 117
Db 1 GTGAGCTGCAGGAGTCGGACCTGTGGCCTCGTGAACCTTCTCAGTCTCTGTCCTCACC 60
Qy 118 TGCAGTCTGCTACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGCGAGTTT 177
Db 61 TGCTCTGCTACTGGCTACTCCTCATCACCAGTGGTTATTACTGGAACTGGATCCGCGAGTTT 120

QY 178 CCAGGAAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCAGTACCTACAC 237
Db 121 CCAGGAAACAACTGGAATGGATGGCTACATAAGCTACGATGGTAGCAATAACTACAAC 180
QY 238 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACAGGTTCTTCTTA 297
Db 181 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACAGGTTCTTCTTA 240
QY 298 CAGTTGAATTTCTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCT 357
Db 241 AAGTTGAATTTCTGACTACTGGGACAGCTCCACATATTACTGTGCGGTTTATTACTAC 300
QY 358 CGGACTACGGCTATGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 301 GATGGTAGTCTTTTGACTACTGGGCGCAAGGACACCGTCACCGTCTCTCTCA 354

RESULT 9
US-09-170-769A-1
; Sequence 1, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIPT1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(639)
US-09-170-769A-1

Query Match 63.3%; Score 260; DB 4; Length 639;
Best Local Similarity 93.2%; Pred. No. 8.2e-80; Mismatches 20; Indels 0; Gaps 0;
Matches 272; Conservative 0;
QY 62 AGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGCA 121
Db 11 AGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCCTCACCTGCA 70
QY 122 CTGTCACTGGCTACTGAATCACAGTGATCATGCTCGAGCTGGATCCGGGAGTTTCCAG 181
Db 71 CTGTCACTGGCTACTGAATCACAGTGATCATGCTCGAGCTGGATCCGGGAGTTTCCAG 130
QY 182 GAAACAACTGGAGTCGAGTGGCTACATAGTTACAGTGGTATCACTACTACACCCAT 241
Db 131 GAAACAGACTGGAGTGGATGGGCTACATAGTTACAGTGGTATCACTACTACACCCAT 190
QY 242 CTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACACAGTTCTTCTCTACAGT 301
Db 191 CTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACACAGTTCTTCTCTACAGT 250
QY 302 TGAATTCGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCT 353
Db 251 TGAATTCGTGACTACTGAGGACACAGCCACATATTACTGTGTAAGAGGGCT 302

RESULT 10
US-08-672-345C-87
; Sequence 87, Application US/08672345C
; Patent No. 5948658

; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-672-345C-87

Query Match 62.8%; Score 258.2; DB 2; Length 366;
Best Local Similarity 84.9%; Pred. No. 2.6e-79;
Matches 303; Conservative 0; Mismatches 48; Indels 6; Gaps 1;
QY 55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCTCTGTGTGAAGCCTTCTCAGTCTCTGTCCCTC 114
Db 1 GATGTGCAGCTTCAGGAGTCGGGACCTGTCTCTGTGTGAAGCCTTCTCAGTCTCTGTCCCTC 60
QY 115 ACCTGCAGCTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGTGGATCCGGCAG 174
Db 61 ACCTGCAGCTGTCACTGGCAATTCATCACCAGTGATCATGCTGGAGTGGATCCGGCAG 120
QY 175 TTTCAGGAAACAAACTGGAGTGGGTGATGATGTTACAGTGGTATCAGTACCTTAC 234
Db 121 TTTCAGGAAACAAACTGGAGTGGGTGATGATGTTACAGTGGTATCAGTACCTTAC 180
QY 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACAGGTTCTTCT 294
Db 181 AACCCCTCTCTCAAAAGTCGAATCTCTATCACTCGAGACAGTCCCAAGAACAGGTTCTTCT 240
QY 295 CTACAGTGGATTTCTGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCCTA 354
Db 241 CTGAGTTGGATTTCTGTGACTCTGAGGACACAGCCACATATTATTGTGTAAGATATCAT 300
QY 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 301 TACTACGGTTCCGGCT-----TACTGGGGCAAGGACTCTGGTCACTGTCTCTGCA 351

RESULT 11
US-09-214-095D-101
; Sequence 101, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US

```
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-101

Query Match      62.8%; Score 258.2; DB 3; Length 366;
Best Local Similarity 84.9%; Pred. No. 2.6e-79;
Matches 303; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

Qy 55 GATGTCAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 114
Db 1 GATGTCAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCTC 60

Qy 115 ACCTGCACTGTCAGTGGTACTCAATCAACAGTGATCATGCTGGAGCTGGATCCGGCAG 174
Db 61 ACCTGCACTGTCAGTGGCAATTCATCAACAGTGATCATGCTGGAGCTGGATCCGGCAG 120

Qy 175 TTTCAGGAACAACCTGAGTGGCTGACATAGTACATAGTACGTTACCTACCTAC 234
Db 121 TTTCAGGAACAACCTGAGTGGCTGACATAGTACATAGTACGTTACCTACCTAGGTAC 180

Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCTGTTTC 294
Db 181 AACCTTCTCTCAATAGTCGAATCTCTATCACTCGAGACACGTCGAAGAACCTGTTTC 240

Qy 295 CTACAGTTGAATCTGTGACTACTGCGGACACGTCCTCAATATTAAGTGAAGATCCCTA 354
Db 241 CTGCAAGTTGAATCTGTGACTACTGCGGACACGTCCTCAATATTAAGTGAAGATATCAT 300

Qy 355 GCTCGGACTACGGCTATGCACTACTGCGGTCAAGAACCTCAGTCACCGTCTCTCA 411
Db 301 TACTACGGTTCGGT-----TACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351

RESULT 12
US-08-554-840-28
; Sequence 28, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..426
US-08-554-840-28

Query Match      62.2%; Score 255.8; DB 3; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.9e-78;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

Qy 1 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCTTCTCGTATCTCTGTCTGATGTG 60
Db 7 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCGGGGTTTCTCTGTACAGGTG 66

Qy 61 CAGCTTCAGAGTCGGGACCTGCTCTGTTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 67 CAGCTTCAGAGTCAGGACCTAGCTCTGTAACCTTCTCAGACTCTGCTCCCTCACCTGT 126

Qy 121 ACTGTCACTGGCTACTCAATCACAGTGATCATGCTCGAGCTGGATCCGGCAGTTTCCA 180
Db 127 TCTGTCACTGGCAGCTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAATTTCCA 183

Qy 181 GGAACAACCTGGAGTGGGTACATAAGTTTACAGTGGTATCATCTACTACAAACCCA 240
Db 184 GGAATAAATTTGAGTACATGGGCTACATAAGTTTACAGTGGTATCATCTACTACAATCCA 243

Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCTGTTCTCTACAG 300
Db 244 TCTCTCAAGAGTCGAATCTCTCACTCGGACACATCCCAAGAACCTGTTCTACTACAA 303

Qy 301 TTGAATTTCTGTGACTACTGGGACACGTCACACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 304 TTGAATTTCTGTGACTACTGGGACACAGGACACATATTACTGTGCTCGCCGAGTTACGGG 363

Qy 361 ACTACGGC-----TATGGACTACTGGGTCAAGAACCTCAGTCACCGTCTCTCA 411
Db 364 AGGACCCGCTACTACTTTGACTTCTGGGGCCAAAGGACCACTCTCACCGTCTCTCA 420

RESULT 13
US-08-925-339-28
; Sequence 28, Application US/08925339
; Patent No. 6440418
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE: 07-NOV-1995
; TELEPHONE: (703) 836-6620
```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 7..426
US-08-925-339-28

Query Match 62.2%; Score 255.8; DB 4; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.9e-78;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;
QY 1 ATGAGAGTGTGCTGATCTTTTGGGCTGTTCACAGCCTTCTCGGTATCTGCTGATGTG 60
DB 7 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCGGGTTTCTGTGACAGGTG 66
QY 61 CAGCTTCAGGAGTCGGACCTGCTGCTGAGGCTTCTCAGTCTCTGCTGCTGCTGCTGCTG 120
DB 67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAACCTTCTCAGACTCTGCTGCTGCTGCTG 126
QY 121 ACTGTCAGTGTCTCAATCACCAGTGTATGCTGAGGCTGATCGGAGCTGATCGGAGCTG 180
DB 127 TCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
QY 181 GGAACAACTGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACCTGCTGCTGCTGCTGCT 300
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QY 301 TTGAATTTCTGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 304 TTGAATTTCTGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 361 ACTAGCGC-----TATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 364 AGGACCCCGTACTACTTTGACTTCTGGGGCCAAGGCACCACTCTCAGCGTCTCCTCA 420

RESULT 14
US-09-332-595-28
Sequence 28, Application US/09332595
Patent No. 6506383
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 7..426
US-09-332-595-28

Query Match 62.2%; Score 255.8; DB 4; Length 426;
Best Local Similarity 79.4%; Pred. No. 1.9e-78;
Matches 331; Conservative 0; Mismatches 77; Indels 9; Gaps 2;
QY 1 ATGAGAGTGTGATCTTTTGGGCTGTTCACAGCCTTCTCGGTATCTGCTGATGTG 60
DB 7 ATGATGGTGTAAAGTCTTCTGTACCTGTTGACAGCCCTTCGGGTTTCTGTGACAGGTG 66
QY 61 CAGCTTCAGGAGTCGGACCTGCTGCTGAGGCTTCTCAGTCTCTGCTGCTGCTGCTGCTG 120
DB 67 CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAACCTTCTCAGACTCTGCTGCTGCTGCTG 126
QY 121 ACTGTCAGTGTCTCAATCACCAGTGTATGCTGAGGCTGATCGGAGCTGATCGGAGCTG 180
DB 127 TCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
QY 181 GGAACAACTGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 184 GGAATAAACTTGAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACCTGCTGCTGCTGCTGCT 300
DB 244 TCTCTCAAGAGTCGAATCTCTATCACTCGAGACATCCAGAACCTGCTGCTGCTGCTGCT 303
QY 301 TTGAATTTCTGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 304 TTGAATTTCTGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 361 ACTAGCGC-----TATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 364 AGGACCCCGTACTACTTTGACTTCTGGGGCCAAGGCACCACTCTCAGCGTCTCCTCA 420

RESULT 15
US-08-672-345C-89
Sequence 89, Application US/08672345C
Patent No. 594858
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE ANTIBODY

NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-672-345C-89

Query Match 61.7%; Score 253.4; DB 2; Length 366;
Best Local Similarity 84.0%; Pred. No. 1.2e-77;
Matches 300; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
QY 55 GATGTGCAGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC 114
Db 1 GACGTGCAGTTGCAGGAGTCGGGACCTGGCCCTGGTGAACCTTCTCAGTCTCTGTCCCTC 60
QY 115 ACCTGCACCTGCACCTGGCTACTCAATCACAGTGATCATGCTGGAGCTGGATCCGGCAG 174
Db 61 ACCTGCACCTGCACCTGGCAATTCAATCACAGTGATCATGCTGGACCTGGATCCGGCAG 120
QY 175 TTTCAGGAACAACTGAGTGGGTGATGGCTACATAAGTTACAGTGGTATCACTACCTAC 234
Db 121 TTTCAGGAACAACTGAGTGGGTGATGGCTACATAAGGCACATTTATGGCACTAGGTAC 180
QY 235 AACCCATCTCTCAAAGTCGAATCTCTATCACTCGAGACACATCCAGAACCAAGTTCTTC 294
Db 181 AACCTTCTCTCATAGTCGAATCTCTATCACTCGAGACACGTCCAGAACCAAGTTCTTC 240
QY 295 CTACAGTTGAATCTGTGACTACTGGGACACGTCACATATTAAGTGCAGATCCCTA 354
Db 241 CTGCAAGTTGGATTCTGTGACTGCTCAGGACACAGCCACATATTATTGTGAAGATATCAT 300
QY 355 GCTCGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 411
Db 301 TACTACGGTTCGGCT-----TACTGGGGCCAAAGGAGCTCTGGTCACTGTCTCTGCA 351

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:39:05 ; Search time 1805.39 Seconds
(without alignments)
5532.953 Million cell updates/sec

Title: US-09-114-285A-30
Perfect score: 411
Sequence: 1 ATGAGAGTGTGATCTTTT.....CCTCAGTCACGGTCTCTCA 411

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	342.2	83.3	693	12	BI456288	BI456288 603172678
2	342	83.2	963	13	BUS24092	BUS24092 AGENCOURT
3	329.8	80.2	502	13	BY007948	BY007948 BY007948
4	329.4	80.1	659	12	BG962947	BG962947 602827932

ALIGNMENTS

RESULT:1
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LOCUS 603172678F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5252131 5', linear EST 21-AUG-2001
DEFINITION mRNA sequence.
ACCESSION BI456288.1 GI:15246944
VERSION BI456288
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 693)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1636 row: 1 column: 20
High quality sequence stop: 691.

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FEATURES                                     Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5252131"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mams"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT      167 a   186 c   174 g   166 t
ORIGIN
Query Match      83.3%; Score 342.2; DB 12; Length 693;
Best Local Similarity 92.3%; Pred. No. 4.5e-89;
Matches 383; Conservative 0; Mismatches 28; Indels 4; Gaps 2;

QY      1  ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCCTGTCGTGATGG 60
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Db      67  ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCCTGTCGTGATGG 126

QY      61  CA-GCTTCAGGAGTCGGGACCTGTCCTGTGTGAAGCTTCTCAGTCTCTGTCCTCACCTG 119
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Db      127  CACGGTTTCAGGAGTCGGGACCTGGCTGTGGAACCTTCTCAGTCTCTGTCCTCACCTG 186

QY      120  CACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGCGAGTTCC 179
      |||
Db      187  CACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGCGAGTTCC 246

QY      180  AGGAACAACCTGGAGTGGGTACATAAGTTACAGTGTATCAGTACCTACCTACAACCC 239
      |||
Db      247  AGGAACAACCTGGAGTGGGTACATAAGTTACAGTGTATCAGTGTAGTACCTACAACCC 306

QY      240  ATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAAGAACCTTCTCTCTACA 299
      |||
Db      307  ATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAAGAACCTTCTCTCTACA 366

QY      300  GTTGAAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGA---TCCTAGC 356
      |||
Db      367  GTTGAAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGAGGGGACTATGG 426

QY      357  TCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
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Db      427  TAACTACATTTGATGGACTACTGGGTCAAGGAACCTTCACTGCGCGTCTCTCTCA 481

RESULT 2
BU524092      963 bp      mRNA      linear      EST 13-SEP-2002
LOCUS
DEFINITION
AGENCOURT_10126646 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6530848 5', mRNA sequence.
ACCESSION
BU524092
VERSION
BU524092.1 GI:22834531
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 963)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM14133 row: d column: 16
High quality sequence stop: 420.

FEATURES                                     Location/Qualifiers
source
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6530848"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      238 a   276 c   220 g   229 t
ORIGIN
Query Match      83.2%; Score 342; DB 13; Length 963;
Best Local Similarity 90.8%; Pred. No. 6e-89;
Matches 376; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY      1  ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCCTGTCGTGATGG 60
      |||
Db      27  ATGAGAGTCTGATCTTTTGTGGCTGTTTCACAGCCTTTCCCTGGTATCCTGTCGTGATGG 86

QY      61  CAGCTTCAGGAGTCGGGACCTGTCCTGTGTGAAGCTTCTCAGTCTCTGTCCTCACCTGC 120
      |||
Db      87  CAGCTTCAGGAGTCAGGACCTGACCTGGTGAACCTTCTCAGTCACTTCACTCACTGC 146

QY      121  ACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGCGAGTTTCCA 180
      |||
Db      147  ACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGCGAGTTTCCA 206

QY      181  GGAACAACCTGGAGTGGGTACATAAGTTACAGTGTATCAGTACCTACCTACAACCCA 240
      |||
Db      207  GGAACAACCTGGAGTGGGTACATAAGTTACAGTGTAGTACCTACAACCCA 266

QY      241  TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAAGAACCTTCTTCTCTACAG 300
      |||
Db      267  TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAAGAACCTTCTTCTCTCAG 326

QY      301  TTGAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATCCCTAGCT--- 357
      |||
Db      327  TTGAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCAAGATATGAGGTAAC 386

QY      358  CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
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Db      387  TAGGACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 440

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RESULT 3
BY007948
LOCUS
DEFINITION
BY007948 RIKEN full-length enriched, B cells CRL-1702 WEHI 231 cDNA
Mus musculus cDNA clone G4D0003J12 5', mRNA sequence.
ACCESSION
BY007948
VERSION
BY007948.1 GI:26068197
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 502)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,

```

Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.J., Reid, J., Ring, M., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sakaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
Nature 420, 563-573 (2002)

MEDLINE
22354683

PUBMED
12466851

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane

T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.

Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.

Sakazume, N., Sakaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami

M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct

Submission

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details..

FEATURES
source

Location/Qualifiers

1. .502

/organism="Mus musculus"

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/cell_type="B cells"

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/clone_lib="RIKEN full-length enriched, B cells CRL-1702

WEHI 231 cDNA"

127 a 126 c 116 g 133 t

BASE COUNT
ORIGIN

Query Match

80.2%; Score 329.8; DB 13; Length 502;

Best Local Similarity 89.5%; Pred. No. 1.6e-85;
Matches 368; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 1 ATGAGAGTGTCTGATTTCTTTTGGCTGCTTTCACAGCCCTTTCTCGTATCTCTGTGATGTG 60
DB 63 ATGAGAGTGTCTGATTTCTTTTGGCTGCTTTCACAGCCCTTTCTCGTATCTCTGTGATGTG 122
QY 61 CAGCTTCAGAGTGTGGACCTGCTGGTGAAGCCTTCTCAGTCTCTGTGCTCCCTCAGCTGC 120
DB 123 CAGCTTCAGAGTGTGGACCTGCTGGTGAAGCCTTCTCAGTCTCTGTGCTCCCTCAGCTGC 182
QY 121 ACTGTCTACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
DB 183 ACTGTCTACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 242
QY 181 GGAACAACAACTGGAGTGGATGGCTACATAAGTTTACAGTGTGTATCTACTACTCAACACCCA 240
DB 243 GGAACAACAACTGGAGTGGATGGCTACATAAGTTTACAGTGTGTATCTACTACTCAACACCCA 302
QY 241 TCTCTCAAAAGTCCGAATCTCTATCAGTGTGGACACATCCCAAGAACACCACTTCTCTACAG 300
DB 303 TCCTCAAAAGTCCGAATCTCTATCAGTGTGGACACATCCCAAGAACACCACTTCTCTACAG 362
QY 301 TTGAATTTCTGTACTCTGGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
DB 363 TTGAATTTCTGTACTCTGGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 417
QY 361 ACTAGCGCTATGTAGTCTGGGCTGAGTGTGTATCTACTACTGGGCAAGGCCACTCTCACAGTCTCTAA 457
DB 418 -GTAAGTCTTGTACTACTGGGCAAGGCCACTCTCACAGTCTCTAA 457

RESULT 4

RG962947

LOCUS

DEFINITION

602827932F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983006 5',

mRNA sequence.

ACCESSION

RG962947

VERSION

BG962947.1 GI:14350584

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 659)

AUTHORS

NIH-NGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Jeffrey B. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLML at:

<http://image.llnl.gov>

Plate: LLAM10986 row: 0 column: 07

High quality sequence stop: 658.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4983006"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI; Site2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 160 a 176 c 161 g 162 t

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES
source

Location/Qualifiers
1..483
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G430007017"
/cell_type="B cells"
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/clone_lib="RIKEN full-length enriched, B cells CRL-1702 WEHI 231 cDNA"

BASE COUNT 119 a 126 c 114 g 124 t

Query Match 78.6%; Score 323.2; DB 10; Length 483;
Best Local Similarity 91.3%; Pred. No. 1.3e-83;
Matches 367; Conservative 0; Mismatches 28; Indels 7; Gaps 2;

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Db 87 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCTTTCTCGGTATCCTGTCTGATGTG 146
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Qy 61 CAGCTTCAGGAGTCGGGA-CCTGTCCTGCTGAAGCCTTCTCAGTCTCTGTCCTCACCTG 119
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Db 147 CAGCTTCAGGAGTCGGGACCTGGCCTGGTGAACCTTCTCAGTCTCTGTCCTCACCTG 206
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Qy 120 CACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCC 179
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Db 267 AGGAACAAACTGGAGTGGGTACATAGCTACAGTGGTATCATCTACACACCC 326
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Qy 240 ATCTCTCAAAAGTCGAATCTCTATCCTCGAGACACATCCAGAACAGTTCTTCTCTACA 299
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Qy 300 GTTGAATTTCTGTACTCTGGGGACACGTCACACATATTACTGTGCAAGATCTATG----- 442
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Db 387 GTTGAATTTCTGTACTCTGGGGACACGTCACACATATTACTGTGCAAGATCTATG----- 442
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Db 443 -GTAAGTACTTGTACTCTGGGGCAAGGCACCTCTCTAC 482
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RESULT 7
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LOCUS 909 bp mRNA linear EST 17-JUL-2001
DEFINITION 602995987F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151932 5', mRNA sequence.
ACCESSION B1249884
VERSION B1249884.1 GI:14797694
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 909)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished

AUTHORS

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM11375 Row: m Column: 21
High quality sequence stop: 840.

FEATURES

Location/Qualifiers

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/clone="IMAGE:5151932"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 207 a 255 c 224 g 223 t

ORIGIN

Query Match 78.2%; Score 321.2; DB 12; Length 909;
Best Local Similarity 87.7%; Pred. No. 7.1e-83;
Matches 363; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
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Db 32 ATGAGAGTGTGATCTTTTGTGGCTGTTTCACAGCCTTTCTCGGTATCCTGTCTGATGTG 91
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Qy 61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
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Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
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Db 272 TCTCTCAAAAGTCGAATCTCTATTTACTCGAGACATCCCAAGAACAGTTCTTCTCTGAG 331
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Qy 301 TTGAATTTCTGTGACTTCTGGGGACACGTCCACATATTACTGTGCAAG---ATCCCTAGCT 357
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Db 332 TTGAATTTCTGTGACTTCTGAGACACAGCCACATATTACTGTGCAAGACCTTCGGGCT 391
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Qy 358 CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTACCCGTTCTCTCA 411
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RESULT 8
BQ922384
LOCUS

853 bp mRNA linear EST 20-AUG-2002

BQ922384

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IMAGE:6477196 5', mRNA sequence.
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VERSION     BQ922384.1
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 853)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14018 row: m column: 05
            High quality sequence stop: 664.
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                /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 Kb. Constructed by Life
            Technologies. Note: this is a NCI CGAP Library."
BASE COUNT  194 a 242 c 196 g 205 t
ORIGIN
Query Match      76.1%; Score 312.8; DB 13; Length 853;
Best Local Similarity 93.7%; Pred. No. 2e-80;
Matches 326; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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DB  24  ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 83
QY  61  CAGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB  84  CAGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCTGTCACCTGC 143
QY  121  ACTGTCAGTGGTACTCAATACCAAGTATCATGCTGGAGCTGGATCGGAGTTTCCA 180
DB  144  ACTGTCAGTGGTACTCCATCACCAAGTATCATGCTGGAGCTGGATCGGAGTTTCCA 203
QY  181  GGAACAAACTCGAGTGGATGGCTACATAGTTACAGTGGTATCACTACCTACAACCCA 240
DB  204  GGAACAAACTCGAGTGGATGGCTACATAGTTACAGTGGTATCACTACCTACAACCCA 263
QY  241  TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTTCTTCTACAG 300
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QY  301  TTGAATTTCTGACTACTCGGGACACGTCACATATTAATTAATTAATTAATTAATTAATTA 348
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RESULT 9
BF582341
LOCUS
DEFINITION  602101173F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:422483 5',
IMAGE:6477196 5', mRNA sequence.
ACCESSION   BF582341
VERSION     BF582341.1
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 910)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9814 row: a column: 20
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                /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI CGAP Library."
BASE COUNT  193 a 239 c 254 g 224 t
ORIGIN
Query Match      76.1%; Score 312.6; DB 10; Length 910;
Best Local Similarity 86.6%; Pred. No. 2.3e-84;
Matches 356; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
QY  1  ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 60
DB  33  ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 91
QY  61  CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
DB  92  CCGCTTCAGGAGTCAGGACCTGGCTGGTGAACCTTCTCAGTCTCTGTCCCTCACCTGC 151
QY  121  ACTGTCAGTGGTACTCAATCACCAGTATCATGCTGGAGCTGGATCGGAGTTTCCA 180
DB  152  ACTGTCAGTGGTACTCTCTTCCAGTGGTATTAATTAATTAATTAATTAATTAATTAATTA 211
QY  181  GGAACAAACTCGAGTGGATGGCTACATAAGTTACAGTGGTATCACTACCTACAACCCA 240
DB  212  GGAACAAACTCGAGTGGATGGCTACATACTCAACAGTGGTATTAAGTACAACCCA 271
QY  241  TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTTCTTCTACAG 300
DB  272  TTTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCAAGAACCAAGTTCTTCTACAG 331
QY  301  TTGAATTTCTGACTACTCGGGACACGTCACATATTAATTAATTAATTAATTAATTAATTA 360
DB  332  TTGAATTTCTGACTACTCGGGACACGTCACATATTAATTAATTAATTAATTAATTAATTA 391
QY  361  ACTACGGCTATGGACTACTCGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
DB  392  CTGTACTACTTTGACTACTCGGGCCCAAGGCCACCCTCTCACAGTCTCTGCA 442
RESULT 10
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BI249876 853 bp mRNA linear EST 17-JUL-2001
LOCUS 602995978F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151882 5',
DEFINITION mRNA sequence.
ACCESSION BI249876
VERSION BI249876.1 GI:14797680
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 853)
COMMENT NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1375 row: k column: 19
High quality sequence stop: 799.
Location/Qualifiers
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/strain="C57BL/6J"
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/tissue type="tumor, gross tissue"
/dev stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 208 a 232 c 200 g 213 t
ORIGIN
Query Match 75.6%; Score 310.6; DB 12; Length 853;
Best Local Similarity 87.2%; Pred. No. 8.7e-80; Mismatches 44; Indels 10; Gaps 2;
Matches 367; Conservative 0;
QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGC-CTTTCCTGGTATCCCTGTCGTATGT 59
DB 25 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCGCTTCTCGTTCTGTCATATGT 84
QY 60 GCAGTTTCAGAGTCGGAGCTGCTCGTGGTGAAGCTTCTCAGTCTCTGTCCTCAGCTG 119
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DB 145 CACTGTCACTGGCTAATCAATCACAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCC 204
QY 180 AGGAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 239
DB 205 AGGAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 264
QY 240 ATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTTACA 299
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QY 300 GTTGAATTTCTGACTACTGGGACACGTCACATATTACTGTGCAAGA-----TC 350
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QY 351 CCTAGCTCGGACTACGGCTATGGAAGTCAAGGAACTCAGTCAACCGTCTCTC 410
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QY 411 A 411
DB 445 A 445
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DEFINITION 602092608F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4207320 5',
DEFINITION mRNA sequence.
ACCESSION BF578272
VERSION BF578272.1 GI:11651984
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 933)
COMMENT NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9769 row: o column: 01
High quality sequence stop: 655.
Location/Qualifiers
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/clone_lib="NCI_CGAP_Co24"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 235 a 261 c 245 g 192 t
ORIGIN
Query Match 71.3%; Score 293; DB 10; Length 933;
Best Local Similarity 93.7%; Pred. No. 1.3e-74;
Matches 327; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCTTCTCGTATCTCTGTCGTATGTG 60
DB 54 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCTTCTCGTATCTCTGTCGTATGTG 112
QY 61 CAGCTTCAGGAGTCGGACCTGCTGGTGAAGCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 113 CAGCTTCAGGAGTCAGACCTGACCTGGTGAAGCTTCTCAGTCTCTCAGTCTCACCTGC 172
QY 121 ACTGTCACTGGTACTCAATCACAGTGATCATGCCCTGGA-GCTGGATCCGGCAGTTTCC 179
DB 173 ACTGTCACTGGTACTCAATCACAGTGATCATGCCCTGGA-GCTGGATCCGGCAGTTTCC 232
QY 180 AGGAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 239
DB 233 AGGAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACTACAAACCC 292
QY 240 ATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCTCTACA 299

Db 293 ATCTCTCAAAAGTCGAATCTCTTACTCGAGACACATCCAAAGACCAAGTCTTCTCTGCA 352
 QY 300 GTTGAATTCGTGACTACTCGGGACACGTCACATATTACTGTGCAAGA 348
 Db 353 GTTGAATTCGTGACTACTCGAGACACAGCCACATATTACTGTGCAAGA 401

RESULT 12
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 LOCUS 602097363F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4217294 5',
 DEFINITION mRNA sequence.
 ACCESSION BF580560
 VERSION BF580560.1 GI:11654272
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 866)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9795 row: n column: 15
 High quality sequence stop: 681.

FEATURES
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 /mol_type="mRNA"
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 /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 Kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 217 a 231 c 220 g 198 t
 ORIGIN

Query Match 71.0%; Score 291.8; DB 10; Length 866;
 Best Local Similarity 91.9%; Pred. No. 2.8e-74;
 Matches 319; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
 QY 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 60
 Db 42 ATGAGAGTCTGATTC-TTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 100
 QY 61 CAGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
 Db 101 CAGCTTCAGGAGTCAGGACCTGGCCTGGTGAACCTTCTCAGTCTCTGTCTGTCACCTGC 160
 QY 121 ACTGTCACTGGGTACTCAATACCAAGTATCATGTGCTGGAGTGGATCGGCGAGTTTCCA 180
 Db 161 ACTGTCACTGGGTACTCCATCACCAGTAGTTATAGCTGGAACCTGGGTCGGCAGTTTCCA 220
 QY 181 GGAACAAACTCGAGTGGGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
 Db 221 GGAACAAACTCGAGTGGGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 280
 QY 241 TCTCTCAAAAGTCGAATCTCTTACTCGAGACACATCCAAAGACCAAGTCTTCTCTACAG 300

Db 281 TCTCTCAAAAGTCGAATCTCTTACTCGAGACACATCCAAAGACCAAGTCTTCTCTGCGAG 340
 QY 301 TTGAATTCGTGACTACTCGGGACACGTCACATATTACTGTGCAAG 347
 Db 341 TTGAATTCGTGACTACTCGAGACACAGCCACATATTACTGTGCGAG 387

RESULT 13
 BF579775 954 bp mRNA linear EST 12-DEC-2000
 LOCUS 602095092F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209454 5',
 DEFINITION mRNA sequence.
 ACCESSION BF579775
 VERSION BF579775.1 GI:11653487
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 954)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9775 row: g column: 23
 High quality sequence stop: 608.

FEATURES
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 /db_xref="taxon:10090"
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Co24"
 /note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 226 a 275 c 247 g 206 t
 ORIGIN

Query Match 70.9%; Score 291.2; DB 10; Length 954;
 Best Local Similarity 84.6%; Pred. No. 4.3e-74;
 Matches 352; Conservative 0; Mismatches 59; Indels 6; Gaps 2;
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 Db 13 ATGAGAGTCTGATTC-TTTGGCTGTTTCACAGCCTTTCCTGGTATCCTGTCGATGTG 71
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 QY 121 ACTGTCACTGGGTACTCAATCAGGAGTATCATGCCTGGAGTGGATCGGCGAGTTTCCA 180
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 QY 181 GGAACAAACTCGAGTGGGTGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
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 QY 241 TCTCTCAAAAGTCGAATCTCTTACTCGAGACACATCCAAAGACCAAGTCTTCTCTACAG 300
 Db 252 TCTCTCAAAAGTCGAATCTCTTACTCGAGACACATCCAGGAACCAAGTCTTCTCTGCGAG 311

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Qy 301 TTGAATCTGTGACTTGGGACACGTCACATATTACTGTGAAGATCCTAGCTCGG 360
Db 312 TTGAATCTGTGACTTGGGACACGTCACATATTATTGTGCAAGACAGATTACTATG 371
Qy 361 ACTAGCGCTA-----TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 411
Db 372 ACAACGAGCTACTTTGACAACCTGGGGCCAAAGCACCACTCTCACAGTCTCCCA 427

RESULT 14
BE309330
LOCUS 601093704F1 NCI_CGAP_Mam5 741 bp mRNA linear EST 26-OCT-2000
DEFINITION 601093704F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:348305 5',
mRNA sequence.
ACCESSION BE309330
VERSION BE309330.1 GI:9167350
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 741)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8527 row: h column: 02
High quality sequence stop: 572.
Location/Qualifiers
1. 741
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:348305"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 171 a 206 c 174 g 190 t
ORIGIN
Query Match 68.1%; Score 279.8; DB 10; Length 741;
Best Local Similarity 87.9%; Pred. No. 8.2e-71;
Matches 305; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGTGATTCTTTTGGCTGTTCACAGCCTTCTCGGTATCCTCTCTGATGTG 60
Db 22 ATGAAAGTTGTAGTCTGTGTACCTGTGTGACAGCCATTCTGGTATCCTGTCTGATGTA 81
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGTGTAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 82 CAGCTTCAGGAGTCAGGACCTGGCCCTCGTGAACCTTCTCAGTCTCTGTCTCTCACCTGC 141
Qy 121 ACTGTCACTGCTACTCAATCACCAGTATCATGCTGGAGCTGATCCGCGAGTTTCCA 180
Db 142 TCTGTCACTGCTACTCCATCACCAGTGGTTATTACTGGAACTGGATCCGGCAATTTCCA 201
Qy 181 GGAAACAACTGGAGTGGGTGCTACATAAGTTTACAGTGTGATCACTACCTACAACCCA 240

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Db 202 GGAAACAACTGGAAATGGATGGGCTACATAAAATTACGACGGTAGCAATAACTACAACCCA 261
Qy 241 TCTCTCAAAAAGTCGAATCTCTATCAGTCGAGACACATCCCAAGAACCAAGTTCTTCTCTACAG 300
Db 262 TCTCTCAAAAAGTCGAATCTCTATCAGTCGAGACACATCTAAGAACCAAGTTTCTCTGAG 321
Qy 301 TTGAATTTCTGTACTACTGTGGGACACGTCACATATTACTGTGTGCAAG 347
Db 322 CTGAATTTCTGTACTACTGTGGGACACAGCTACATATTACTGTGTGCAAG 368

RESULT 15
BE963270
LOCUS 602828371F1 NCI_CGAP_Co24 735 bp mRNA linear EST 12-JUN-2001
DEFINITION 602828371F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:498352 5',
mRNA sequence.
ACCESSION BE963270
VERSION BE963270.1 GI:14950907
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 735)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10987 row: m column: 17
High quality sequence stop: 551.
Location/Qualifiers
1. 735
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:498352"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 172 a 218 c 169 g 176 t
ORIGIN
Query Match 65.9%; Score 271; DB 12; Length 735;
Best Local Similarity 87.2%; Pred. No. 3.1e-68;
Matches 355; Conservative 0; Mismatches 45; Indels 7; Gaps 5;

Qy 1 ATGAGAGTGTGATTCTTTTGGCTGTTCACAGCCTTCTCGGTATCCTGTCTGATGTG 60
Db 29 ATGAGAGTGTCTATTCTTTTGGCTGTTCACAGCCTTCTCGGTATCCTGTCTGATGTG 88
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 89 CAGCTTCAGGAGTCAGGACCTGGCCCTGGTGAACCTTCTCAGTCTCTGTCCCTCACCTGC 148
Qy 121 ACTGTCACTGCTACTCAATCACCAG--TGATCATGCTGGAGCTGGATCCGCGAGTTTCC 179
Db 149 ACTGTCACTGCTACTCCATCACCAGCTGGTTATTACTGGAACTGGATCCGCGAGTTTCC 208
Qy 180 AGAAACAACTGGAGTGGATGGGCTACA--TAAGTTACAGTGGTATCACTACCTACAACC 238

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Db 209 AGGAAACAACTGGAGTGGGCTACACTATATAATAGTGGTAGCACTAACTACAACC 268
Qy 239 CATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCCTAC 298
Db 269 CATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGAACCAAGTTCTTCCTGC 328
Qy 299 AGTTG-AATTCTGTGACTACTGGGGACAC-GTCCACATATTACTGTGCAAGATCCCTAGC 356
Db 329 AGTTGCACCTTCTGTGACGACTGAGGACACAGCCACATATTACTGTGCAAG---TGGAGG 385
Qy 357 TCGGACTAGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCG 403
Db 386 GGGTAAGGGATACTTTGACTACTGGGGCCAGGCCACCACCTCTCACGG 432

Search completed: October 24, 2003, 05:48:32
Job time : 1810.39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 02:25:30 ; Search time 204.462 Seconds
(without alignments)
5426.282 Million cell updates/sec

Title: US-09-114-285A-30

Perfect score: 411

Sequence: 1 ATGAGAGTGTGATCTTTT.....CCTCAGTCACCGTCTCCTCA 411

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	13	AAQ30756
2	322	78.3	408	21	AAA74604
3	316.8	77.1	402	25	ABZ23940
4	313.4	76.3	408	17	AAT40804
5	313.4	76.3	408	19	AAV12261
6	297.8	72.5	357	18	AAT58258
7	284.6	69.2	836	16	AAT04584
8	284.6	69.2	836	21	AAZ51113

9	283	68.9	836	15	AAQ66698	Sequence of the si
10	281.2	68.4	1200	20	AX90424	Chimeric antibody
11	281.2	68.2	357	25	ABZ21158	Variable region an
12	279.2	67.9	720	14	AAQ40462	Fv(TU27). Homo sa
13	277	67.4	357	25	ABZ21157	Variable region an
14	274.6	66.8	378	13	AAQ25667	Sequence of the an
15	272.8	66.4	714	15	AAQ67358	Anti-traseolide 02
16	269	65.5	354	25	ABZ57952	Humanised antibody
17	267	65.0	1002	21	AAA50164	DNA encoding SH7 s
18	266.2	64.8	363	21	AAA50159	Antibody SH7 heavy
19	265.8	64.7	357	25	ABZ21160	Variable region an
20	264.4	64.3	354	17	AAT39555	Variable heavy cha
21	264.4	64.3	354	18	AAT69539	Anti-human FasL an
22	260.8	63.5	411	21	AAA30416	Mouse VH group I(A
23	260	63.3	639	16	AAQ80291	Monoclonal antibod
24	259.4	63.1	354	25	ABZ57951	Humanised antibody
25	258.2	62.8	366	19	AAV09790	DNA encoding the h
26	257.8	62.7	354	25	ABZ57950	Humanised antibody
27	255.8	62.2	426	18	AAT73902	Variable heavy sub
28	255.8	62.2	426	20	AAZ28410	Antibody 24-31 hum
29	255.8	62.2	426	24	ABX03771	Murine wild-type a
30	253.4	61.7	366	19	AAV09792	DNA encoding the h
31	250.4	60.9	746	18	AAT62573	scFv(1.1ASML) gene
32	250.2	60.9	351	11	AAQ06214	VH domain of antib
33	250.2	60.9	351	17	AAT63503	Monoclonal antibod
34	250.2	60.9	351	17	AAT36663	Monoclonal antibod
35	245.6	59.8	420	19	AAV09801	DNA encoding the h
36	245.4	59.7	420	19	AAV09803	DNA encoding the h
37	244.8	59.6	847	21	AAQ96550	Nucleotide sequenc
38	244	59.4	830	13	AAQ30714	Sequence of PCR pr
39	243.8	59.3	1135	22	AAV76338	Anti-VHSV single c
40	243.4	59.2	2010	20	AAV99657	Fusion protein L49
41	242.4	59.0	798	13	AAQ30706	Sequence of Clone
42	242.4	59.0	798	15	AAQ44642	Rd phage clone seq
43	236.6	57.6	426	18	AAT73900	Humanised variable
44	236.6	57.6	426	20	AAZ28408	Antibody 24-31 hum
45	236.6	57.6	426	24	ABX03769	Murine humanised a

ALIGNMENTS

RESULT 1
AAQ30756
ID AAQ30756 standard; cDNA; 411 BP.

XX AC AAQ30756;
XX DT 25-MAR-2003 (updated)
XX DT 30-MAR-1993 (first entry)

DE pPM-h1.

XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
XX heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
XX plasmid; pPM-k3; pPM-h1; ss.

XX Synthetic.

XX Key sig_peptide Location/Qualifiers
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FT 55..411 /*tag= b
FT mat_peptide

XX WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP00544.

XX 25-APR-1991; 91JP-0095476.

PR 19-FEB-1992; 92JP-0032084.

AB223940
 ID AB223940 standard; DNA; 402 BP.
 XX
 AC AB223940;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Antibody 806 variable heavy chain (VH) region encoding DNA.
 XX
 KW Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;
 KW monoclonal antibody; mAb 806; antibody therapy; tumour; gene; ds.
 XX
 OS Homo sapiens.
 XX
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 FT mat_peptide 55..402
 FT /*tag= c
 FT /*note= "806 VH region"
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 WO200292771-A2.
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 PD 21-NOV-2002.
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 PF 13-MAY-2002; 2002WO-US15185.
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 PR 11-MAY-2001; 2001US-290410P.
 PR 28-SEP-2001; 2001US-326019P.
 PR 21-DEC-2001; 2001US-342258P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritter G;
 PI Jungbluth A, Stockert E, Collins P, Caveness WK, Huang H;
 PI Burgess AW, Nice EC;
 XX
 DR WPI; 2003-129282/12.
 DR P-PSDB; ABB82796.
 XX
 PT Novel specific binding members, particularly antibodies recognizing
 PT epidermal growth factor receptor epitope found only in tumorigenic
 PT cells, useful for diagnosing, preventing and treating cancer in mammals
 XX
 PS Claim 40; Fig 14A; 123pp; English.
 XX
 CC The invention relates to an isolated specific binding member (I) which
 CC recognizes an epidermal growth factor receptor (EGFR) epitope which is
 CC found in tumorigenic, hyperproliferative or abnormal cells and not
 CC detectable in normal cells. The EGFR epitope is located within the region
 CC comprising residues 273-501 of EGFR and does not demonstrate any amino
 CC acid sequence alterations or substitutions from normal EGFR. (I) is
 CC capable of binding the de2-7 EGFR at an epitope distinct from the
 CC junctional peptide and does not bind to EGFR on normal cells in the
 CC absence of aberrant expression, or in the absence of amplification of
 CC normal wild-type gene. The binding member comprises the VH and VL
 CC polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for
 CC treating or diagnosing human or animal body, especially for treating
 CC tumour in a human. (I) is useful for the preparation of a medicament and
 CC for preventing or treating cancer which is located in or adjacent the
 CC brain, in a mammal. (I) is also useful for detecting the presence of
 CC amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation; where
 CC EGFR is measured by contacting a biological sample from a mammal in which
 CC the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose
 CC glycosylation is suspected with (I) under conditions that allow binding
 CC of the EGFR to the antibody to occur, and detecting whether binding has
 CC occurred between the EGFR from the sample and the antibody, where the
 CC detection of binding indicates that presence or activity of the EGFR in
 CC the sample. This method is useful for detecting cancer in mammals by
 CC detecting the presence or activity of an EGFR which indicates the

CC existence of a tumour or cancer in the mammal. A pharmaceutical
 CC composition comprising (I), and optionally vehicle, carrier or diluent is
 CC useful for preventing and/or treating cancer in mammals, especially for
 CC treating brain-resident cancers that produce aberrantly expressed EGFR in
 CC mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic
 CC astrocytoma or neoplastic arteriovenous malformations, and malignant
 CC neural tumours in mammals. The present sequence represents the mAb 806
 CC VH region encoding DNA.
 XX
 SQ Sequence 402 BP; 91 A; 102 C; 97 G; 112 T; 0 other;
 Query Match 77.1%; Score 316.8; DB 25; Length 402;
 Best Local Similarity 88.0%; Pred. No. 1.3e-89;
 Matches 345; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGTGATTTCTTTTGGCTGTTTCACAGCCTTTCTCGTATCTCTGTGATGTG 60
 DB 1 ATGAGAGTGTGATTTCTTTTGGCTGTTTCACAGCCTTTCTCGTATCTCTGTGATGTG 60
 QY 61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
 DB 61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
 QY 121 ACTGTCACTGGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
 DB 121 ACTGTCACTGGCTACTCAATCACCAGTATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180
 QY 181 GGAACAACACTGGAGTGGGCTACATAAGTTACAGTGGTATCAGTCTACCTACCAACCCA 240
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 DB 301 TTGAATTTCTGTGACTATTGAGGACACAGCCACATATTTACTGTGTAAACGGCGGCGGG 360
 QY 361 ACTACGGCTATGGACTACTCGGGTCAAGGAAC 392
 DB 361 TTCTCTTATTGGGGCCAAAGGAACTCTGGTCAAC 392
 RESULT 4
 AAT40804
 ID AAT40804 standard; cDNA to mRNA; 408 BP.
 XX
 AC AAT40804;
 XX
 DT 10-FEB-1997 (first entry)
 XX
 DE MAb 1.4 heavy chain, directed against type II phospholipase A2.
 XX
 KW Monoclonal antibody; phospholipase; myocardial infarction;
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;
 KW chronic rheumatism; adult respiratory distress syndrome;
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma;
 KW ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 CDS 1..408
 FT /*tag= a
 FT /product= Monoclonal antibody heavy chain.
 XX
 PN WO9620959-A1.
 XX
 PD 11-JUL-1996.
 XX
 PF 27-DEC-1995; 95WO-JP02714.
 XX

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PR 29-DEC-1994; 94JP-0340006.
XX (YAMA ) YAMANOUCHI PHARM CO LTD.
XX Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;
PI WPI; 1996-333946/33.
DR P-PSDB; AAW01144.
XX Monoclonal antibody inhibiting type II phospholipase A2 activity -
PT for treatment of myocardial and cerebral infarction
XX Example 6; Figure 11; 69pp; Japanese.
XX Monoclonal antibodies which inhibit type II phospholipase A2 are
CC useful in the treatment of myocardial infarction, cerebral
CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,
CC pancreatitis, adult respiratory distress syndrome and colitis. The
CC antibodies were generated by immunising Balb/C mice with recombinant
CC human type II phospholipase A2. Spleen cells from the mice were
CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas
CC obtained were screened for phospholipase A2 inhibitory activity.
CC Active clones were isolated including 12H5, 1.4 and 10.1. These
CC were cultured and the antibody isolated from the culture
CC supernatant by precipitation with ammonium sulphate and purification
CC on a column of protein A-Sepharose CL4B. Because the antibody acts
CC on the primate and mouse forms of enzyme as well as human it is
CC particularly suitable for preclinical testing.
XX Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
SQ
Query Match 76.3%; Score 313.4; DB 17; Length 408;
Best Local Similarity 86.9%; Pred. No. 1.5e-88;
Matches 357; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTACAGCCTTTTCCGTGATCTCTGTGATGTG 60
DB 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTACAGCCTTTTCCGTGATGTG 60
QY 61 CAGCTTCAGAGTCGGGACCTGCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 61 CAGCTTCAGGAATCGGGACCTGGCTGGTGAACCTTCTCAATCTCTGTCCTCACCTGC 120
QY 121 ACTGTCACCTGGCTACTCAATCACCAGTGTATGCTGGAGTGGATCCGGCAGTTTCCA 180
DB 121 ATGGTCACTGGCTACTCAATCACCAGTGTATGCTGGAGTGGATCCGGCAGTTTCCG 180
QY 181 GGAACAAACTCGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
DB 181 GGAACAAACTCGAGCGGATGGATACATAAGGTACAGTGGTTACACTAGCTACCAACCCA 240
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGCAGTCTTCTCTACG 300
DB 241 TCTCTCAAAAGTCGAATCTTTATCAGCGGAGACACATCCCAAGCAGTCTTCTCTACAT 300
QY 301 TTGAATTCGTGACTACTCGGACAGCTCCACATATTACTGTGCAAGTCCCTAGCTCGG 360
DB 301 TTGACTTCTGTGACTACTGAGACACAGCCACATATTACTGTACAGAGACTTGG---AC 357
QY 361 ACTACGGCTATGACTACTCTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 358 GCCTGTACTTCGATGTTTGGGGCGGAGGACCAACGGTCACCGTCTCCTCA 408
RESULT 5
AAV12261
ID AAV12261 standard; cDNA to mRNA; 408 BP.
AC AAV12261;
XX Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.
DT 16-JUN-1998 (first entry)
XX
```

```
XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
KW amelioration; kidney disorder; nephrotoxicity; anticancer; ds.
XX Unidentified.
OS Key Location/Qualifiers
FH 1..408
FT /*tag= a
FT /product= "monoclonal antibody 1.4 heavy chain"
FT /note= "no stop codon given"
XX WO9749427-A1.
XX 31-DEC-1997.
XX 27-JUN-1997; 97WO-JP02241.
XX 19-SEP-1996; 96JP-0247635.
XX 27-JUN-1996; 96JP-0167286.
XX (YAMA ) YAMANOUCHI PHARM CO LTD.
XX Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;
PI WPI; 1998-076914/07.
DR P-PSDB; AAW44169.
XX Amelioration of kidney disorders caused by cisplatin administration
PT - by treatment with an antibody inhibiting type II phospholipase A2
PT activity
XX Disclosure; Page 36-37; 74pp; Japanese.
XX The present sequence encodes the monoclonal antibody 1.4 heavy chain
CC against type II phospholipase A2, from the present invention. The
CC present invention describes a novel method for the amelioration of
CC kidney disorders (such as acute renal failure) associated with the
CC administration of cisplatin for the treatment of cancer. The method
CC comprises treatment with a monoclonal antibody which inhibits the
CC activity of type II phospholipase A2 (particularly of type II
CC phospholipase A2 of human origin), or with a protein or peptide
CC possessing the same inhibitory activity and containing a part of the
CC antibody sequence. Preferably the antibody also inhibits the activity of
CC ape and/or mouse type II phospholipase A2, and has the ability to
CC release type II phospholipase A2 bound to a cell membrane. Three
CC specific monoclonal antibodies having these properties which can be
CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,
CC FERM BP-5298 and FERM BP-5297, respectively. The method can be used for
CC suppressing the nephrotoxicity which is a characteristic feature of
CC cisplatin administration, and therefore allowing more efficient use of
CC this drug as an anticancer agent, e.g. by allowing an increased dosage
CC to be used.
XX Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
SQ
Query Match 76.3%; Score 313.4; DB 19; Length 408;
Best Local Similarity 86.9%; Pred. No. 1.5e-88;
Matches 357; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTACAGCCTTTTCCGTGATCTCTGTGATGTG 60
DB 1 ATGAGAGTCTGATCTTTTGTGGCTGTTTACAGCCTTTTCCGTGATGTG 60
QY 61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCTGC 120
DB 61 CAGCTTCAGGAATCGGGACCTGGCTGGTGAACCTTCTCAATCTCTGTCCTCACCTGC 120
QY 121 ACTGTCACCTGGCTACTCAATCACCAGTGTATGCTGGAGTGGATCCGGCAGTTTCCA 180
DB 121 ATGGTCACTGGCTACTCAATCACCAGTGTATGCTGGAGTGGATCCGGCAGTTTCCG 180
QY 181 GGAACAAACTCGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACCTACCAACCCA 240
DB 181 GGAACAAACTCGAGCGGATGGATACATAAGGTACAGTGGTTACACTAGCTACCAACCCA 240
QY 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGCAGTCTTCTCTACG 300
DB 241 TCTCTCAAAAGTCGAATCTTTATCAGCGGAGACACATCCCAAGCAGTCTTCTCTACAT 300
QY 301 TTGAATTCGTGACTACTCGGACAGCTCCACATATTACTGTGCAAGTCCCTAGCTCGG 360
DB 301 TTGACTTCTGTGACTACTGAGACACAGCCACATATTACTGTACAGAGACTTGG---AC 357
QY 361 ACTACGGCTATGACTACTCTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
DB 358 GCCTGTACTTCGATGTTTGGGGCGGAGGACCAACGGTCACCGTCTCCTCA 408
RESULT 5
AAV12261
ID AAV12261 standard; cDNA to mRNA; 408 BP.
AC AAV12261;
XX Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.
DT 16-JUN-1998 (first entry)
XX
```


Db 181 GGAACAACTGGAGCGGATGGGATACATAAGGTACAGTGGTTACACTAGCTCAACCCCA 240
 Qy 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTCTCTACAG 300
 Db 241 TCTCTCAAAAGTGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTCTCTACAT 300
 Qy 301 TTGAATTTCTGTACTACTGGGGACACGTCCACATATTACTGTGTGAAGATCCCTAGTCTGG 360
 Db 301 TTGAATTTCTGTACTACTGGGGACACACATATTACTGTGTGAAGATCCCTAGTCTGG 360
 Qy 361 ACTACGGCTATGGACTACTGGGTCAAGGACCTCAGTCACCGTCTCCTCA 411
 Db 358 GCCTGGTACTTCGATGTTTGGGGCGCAGGGACAAACGTCACCGTCTCCTCA 408

RESULT 6

AAT58258

ID AAT58258 standard; cDNA; 357 BP.

XX AC

AAT58258;

XX AC

22-AUG-1997 (first entry)

XX DT

XX DE

Lead binding MAB 13D10 heavy chain variable region encoding cDNA.

XX KW

Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;

XX KW

pharmaceutical; health care; skin treatment; pesticide; herbicide;

XX KW

heavy metal; ss.

XX OS

Mus musculus.

XX XX

XX Key

Location/Qualifiers

XX CDS

1..357

/*tag= a

/note= "no stop codon given"

XX FT

XX FT

XX PN

WO9639518-A1.

XX XX

12-DEC-1996.

XX PD

XX XX

05-JUN-1996; 96WO-US09258.

XX PF

XX XX

10-OCT-1995; 95US-0541373.

XX PR

05-JUN-1995; 95US-0462798.

XX PR

XX XX

(BION-) BIONEERASKA INC.

XX PA

XX XX

Lopez O, Murray PJ, Wylie DE;

XX PI

XX XX

WPI; 1997-043140/04.

XX DR

XX DR

P-PSDB; AAW01584.

XX DR

XX XX

DNA encoding heavy metal binding polypeptide sequences - used for

XX PT

detecting, removing, adding or neutralising heavy metals, such as

XX PT

XX PT

XX PT

XX PT

XX PT

XX PS

XX PS

XX XX

SQ

Query Match 72.5%; Score 297.8; DB 18; Length 357;
 Best Local Similarity 89.6%; Pred. No. 1.2e-83;
 Matches 320; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 Qy 55 GATGTGACGCTTCAGGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGTCCCTC 114
 Db 1 GATGTGACGCTTCAGGAGTCGGGACCTGCTCGTGAAGCCTTCTCAGTCTCTGTCCCTC 60
 Qy 115 ACCTGCACTGTCTACTGGTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCCGGCAG 174
 Db 61 ACCTGCACTGTCTACTGGTACTCAATCACCAGTGATCATGCTCGGAGCTGGATCCGGCAG 120
 Qy 175 TTTCCAGGAAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCATCTACCTAC 234
 Db 121 TTTCCAGGAAACAACTGGAGTGGGTACATAAGTTACAGTGGTATCATCTACCTAC 180
 Qy 235 AACCCATCTCTCAAAAGTCGAATCTATCACTCGAGACACATCCAGAACCAAGTCTCTC 294
 Db 181 AACCCATCTCTCAAAAGTCGAATCTATCACTCGAGACACATCCAGAACCAAGTCTCTC 240
 Qy 295 CTACAGTTGAATTTCTGTGACTACTGGGGACACAGTCCACATATTACTGTGCAAGATCCCTA 354
 Db 241 CTGCAAGTTGAATTTCTGTGACTACTGGGGACACAGTCCACATATTACTGTGCAAGATCCCTA 300
 Qy 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACTCAGTCAAGTCTCTCTCA 411
 Db 301 AACTACCCGGTGTACTTTGACTACTGGGGCAAGGCACCACTCTCACAGTCTCTCTCA 357
 RESULT 7
 AAT04584
 ID AAT04584 standard; DNA; 836 BP.
 XX AC
 AC AAT04584;
 XX DT
 DT 09-APR-1996 (first entry)
 XX DE
 DE AntiDNP-scFv.
 XX KW
 KW Antibody; scFv; targeting peptide; retroviral vector; gene therapy;
 KW adenosine deaminase deficiency; ADA; cancer; hapten dinitrophenol; ss.
 XX OS
 OS Synthetic.
 XX PN
 PN WO9523846-A1.
 XX PD
 PD 08-SEP-1995.
 XX PF
 PF 03-MAR-1995; 95WO-US02537.
 XX PR
 PR 04-MAR-1994; 94US-0205980.
 XX PA
 PA (UYNE-) UNIV NEW JERSEY.
 XX PI
 PI Dornburg RC;
 XX DR
 DR WPI; 1995-320563/41.
 XX PT
 PT Retroviral vectors for use in cell specific gene transfer - contain
 PT antibody-envelope and wild-type envelope-fusion proteins
 XX PS
 PS Example; Fig 3; 35pp; English.
 XX CC
 CC The anti-hapten dinitrophenol single chain antibody (anti-DNP scFv)
 CC encoded by this sequence is used as a targeting peptide (TP), which is
 CC fused to the envelope protein of a retroviral vector. When the TP is
 CC fused to the envelope protein, it replaces or disrupts the natural
 CC receptor binding site. By using a TP that recognises a cell surface
 CC antigen, the retroviral vectors containing TP's can be used in a cell
 CC type specific method for introducing genes into cells. These retroviral
 CC vectors can be used in the gene therapy of human genetic diseases
 CC including, adenosine deaminase (ADA) deficiency, and in clinical trials


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Db 254 TCTCTCAAAAATCGAATCTCCATCTCGTGACACATCTAAGAACCGATTTTCTCTGAAG 313
Qy 301 TTGAATTTCTGCTACTACTGGGACACAGCTCCACATATTACTGTGCAAGATCCCTAG---CT 357
Db 314 TTGAATTTCTGCTACTACTGGGACACAGCTCCATATTACTGTGCAAGAGATAGAGGGTAT 373
Qy 358 CGGACTACGGCTATGAGCTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 374 GACCACGGGGGTTTGCTTACTGGGGCCAAGGAGCTCTGGTCACTGTCTCTGCA 427

RESULT 11
ID ABZ21158 standard; DNA; 357 BP.
XX ABZ21158;
XX
XX 28-MAR-2003 (first entry)
XX
DE Variable region anti-bisphenol A antibody chain coding sequence #2.
XX
XX Variable region; anti-bisphenol A; antibody; murine; heavy chain;
KW light chain; gene; ds.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..357
XX FT /*tag= a
XX FT /partial
XX FT /product= "Variable region anti-bisphenol A antibody
* FT chain #2"
XX FT /note= "No start or stop codon given"
XX
XX JP2002253259-A.
XX
XX 10-SEP-2002.
XX
XX 02-MAR-2001; 2001JP-0058673.
XX
XX 02-MAR-2001; 2001JP-0058673.
XX
XX (BIOS-) BIO APPLIED SYSTEMS KK.
XX
XX WPI: 2003-096537/09.
XX P-PSDB; ABB98906.
XX
XX Gene encoding anti-bisphenol A antibody, a recombinant protein and its
XX preparation, a DNA, a vector, a transformant, preparation of a
XX recombinant protein, a kit for determining bisphenol A -
XX
XX Claim 1; Page 11; 19pp; Japanese.
XX
XX The present invention relates to sequences for murine heavy chain
XX variable region or light chain variable region of anti-bisphenol A
XX antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are
XX useful for the preparation of recombinant protein.
XX
XX Sequence 357 BP; 94 A; 92 C; 79 G; 92 T; 0 other;
XX
XX Query Match 68.2%; Score 280.2; DB 25; Length 357;
XX Best Local Similarity 86.6%; Pred. No. 4.1e-78;
XX Matches 309; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
XX
Qy 55 GATGTGACGTTTCAGGAGTCGGGACCTGTCTGTGTTCAAGCCCTTCTCAGTCTCTGTCCTC 114
Db 1 GATGTGACGTTTCAGGAGTCAGGACCTGTGCTCGTGAACCTTCTCAGTCTCTGTCCTC 60
Qy 115 ACCTGCAGTCTGCTGGTCTACTCAATCACCAGTATCATGCTGTGAGCTGGATCCGGCAG 174
Db 61 ACCTGCTCTGCTGGTCTACTCCATCACCAGTGTATTACTGGAACCTGGATCCGGCAG 120
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTAC 234

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Db 121 TTTCAGGAAACAACTGGAATGGATGGCTTACATAAGGTACGAGGTAGCAATAACTAC 180
Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCTACTCGAGACACATCCAAGAACCGATTCTTC 294
Db 181 AACCCATCTCTCAAAATCGAATCTCCATCTACTCGTGACACATCTAAGAACCGATTTTTC 240
Qy 295 CTACAGTTGAATTTCTGTGACTACTGGGACACGTCACACATATTACTGTGCAAGATCCCTCA 354
Db 241 CTGAAGTTGAATTTCTGTGACTACTGAGACACAGTACATATTACTGTGCAAGATATTG 300
Qy 355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
Db 301 GGACGGGGCTATGTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 357

RESULT 12
ID AAQ40462 standard; DNA; 720 BP.
XX AAQ40462;
XX
XX 25-MAR-2003 (updated)
XX 20-AUG-1993 (first entry)
XX
XX Fv(TU27).
XX
XX pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
XX heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
XX immunomodulator; immunosuppressant; graft rejection; allergy;
XX autoimmune disease; leukemia; cyclosporin; ss.
XX
XX Homo sapiens.
XX
XX EP539748-A1.
XX
XX 05-MAY-1993.
XX
XX 30-SEP-1992; 92EP-0116746.
XX
XX 03-OCT-1991; 91JP-0256335.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX Hamuro J, Shimamura T, Taki S;
XX
XX WPI; 1993-145163/18.
XX P-PSDB; AAR34510.
XX
XX Polypeptide(s) which bind H chain of human IL-2 receptors - for
XX treating inflammatory, allergic and auto-immune disorders,
XX leukaemias etc.
XX
XX Claim 6; Page 20; 27pp; English.
XX
XX The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
XX polypeptides consisting only of the V regions were purified and
XX sequenced. The polypeptides are capable of binding to the beta
XX chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
XX receptor. They are useful as immunomodulators and
XX immunosuppressants, e.g. to prevent graft rejection or to treat
XX inflammatory allergic and autoimmune diseases, or leukemia. Unlike
XX cyclosporin etc., they are both effective and safe.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 720 BP; 186 A; 188 C; 170 G; 176 T; 0 other;
XX
XX Query Match 67.9%; Score 279.2; DB 14; Length 720;
XX Best Local Similarity 88.5%; Pred. No. 1.1e-77;
XX Matches 315; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
XX
Qy 56 ATGTGACGTTTCAGGAGTCGGGACCTGTCTGTGTTGAAGCCCTTCTCAGTCTCTGTCCTCA 115

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Db 368 AGGTCAAACTCGAGGAGTCTGGACCTGGCCCTGGTGAACCTTCTCAGTCTCTGTCCCTCA 427
 QY 116 CCTGACCTGTCACTGGCTACTCAATCACCAGTGTATGCTCGAGCTGGATCGGCAGT 175
 Db 428 CCTGACCTGTCACTGGCTACTCAATCACCAGTGTATGCTCGAGCTGGATCGGCAGT 487
 QY 176 TTCCAGGAAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACCTACA 235
 Db 488 TTCCAGGAAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACCTACA 547
 QY 236 ACCCATCTCTCAAAAGTCGAATCTCTATCATCTGAGACACATCCAAAGACAGTTCTTCC 295
 Db 548 ACCCATCTCTCAAAAGTCGAATCTCTATCATCTGAGACACATCCAAAGACAGTTCTTCC 607
 QY 296 TACAGTTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAG 355
 Db 608 TGCAGTTGAATCTGTGACTACTGAGACACGTCACATATTACTGTGCAAGA---GGTG 664
 QY 356 CTCGGACTACGGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
 Db 665 GTTTCCTCTATGCTATGGACTACTGGGCTCAAGGACACCGTCACCGTCTCTCTCA 720

RESULT 13
 ABZ21157
 ID ABZ21157 standard; DNA; 357 BP.
 XX AC ABZ21157;
 XX DT 28-MAR-2003 (first entry)
 XX DE Variable region anti-bisphenol A antibody chain coding sequence #1.
 XX KW Variable region; anti-bisphenol A; antibody; murine; heavy chain;
 XX KW light chain; gene; ds.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT CDS 1..357
 FT /*tag= a
 FT /partial
 FT /product= "Variable region anti-bisphenol A antibody
 chain #1"
 FT /note= "No start or stop codon given"
 XX PN JP2002253259-A.
 XX PD 10-SEP-2002.
 XX PF 02-MAR-2001; 2001JP-0058673.
 XX PR 02-MAR-2001; 2001JP-0058673.
 XX PA (BIOS-) BIO APPLIED SYSTEMS KK.
 XX DR WPI; 2003-096537/09.
 DR P-FSDB; ABB98905.
 XX Gene encoding anti-bisphenol A antibody, a recombinant protein and its
 PT preparation, a DNA, a vector, a transformant, preparation of a
 PT recombinant protein, a kit for determining bisphenol A -
 XX Claim 1; Page 10; 19pp; Japanese.
 XX The present invention relates to coding sequences for murine heavy chain
 CC variable region or light chain variable region of anti-bisphenol A
 CC antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are
 CC useful for the preparation of recombinant protein.
 XX Sequence 357 BP; 94 A; 91 C; 79 G; 93 T; 0 other;
 SQ Query Match 67.4%; Score 277; DB 25; Length 357;

Best Local Similarity 86.0%; Pred. No. 4.2e-77;
 Matches 307; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 55 GATGTGAGCTTCAGGAGTCGGACCTGCTCGTGAAGCTTCTCAGTCTCTGTCCCTC 114
 Db 1 GATGTGAGCTTCAGGAGTCGGACCTGCTCGTGAAGCTTCTCAGTCTCTGTCTCTC 60
 QY 115 ACCTGCACCTGCTACTGGCTACTCAATCACCAGTGATCATCGCTGGAGCTGGATCCGCGAG 174
 Db 61 ACCTGCTCTGCTACTGGCTACTCAATCACCAGTGGTTATTACTTGAAGTGGATCCGCGAG 120
 QY 175 TTTCAGGAAACAACTGGAGTGGGCTACATAAGTTACAGTGGTATCACTACCTAC 234
 Db 121 TTTCAGGAAACAACTGGAGTGGGCTATATAAGTACGACCGTAGCAATAACTAC 180
 QY 235 AACCCATCTCTCAAAAGTCGAATCTCTATCATCTGAGACACATCCAAAGACAGTTCTTTC 294
 Db 181 AACCCATCTCTCAAAAGTCGAATCTCTATCATCTGAGACACATTAAGAACAGGATTTTC 240
 QY 295 CTACAGTTGAATCTGTGACTACTGGGACACAGCTCCACATATTACTGTGCAAGATCCCTA 354
 Db 241 CTGAATTTGAATCTGTGACTCTCTGAGGACACAGCTACATATTACTGTGCAAGATTTG 300
 QY 355 GCTCGGACTACGGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
 Db 301 GGACGGGCTATGTTGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCTCA 357

RESULT 14
 AAQ25667
 ID AAQ25667 standard; cDNA; 378 BP.
 XX AC AAQ25667;
 XX DT 25-MAR-2003 (updated)
 DT 28-DEC-1992 (first entry)
 XX DE Sequence of the anti-urokinase antibody kappa variable region (VK)
 DE cDNA.
 XX KW Chimeric monoclonal antibody; anti-urokinase antibody; PCR;
 KW antithrombotic agent; myocardial infarction therapy; ss.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT sig_peptide 1..9
 FT /*tag= a
 FT mat_peptide 10..378
 FT /*tag= b
 FT misc_feature 1..27
 FT /*tag= c
 FT misc_feature 18..32
 FT /label= VH01 primer
 FT /*tag= d
 FT misc_feature 340..371
 FT /label= 5'VH1 primer
 FT /*tag= e
 FT misc_feature 356..371
 FT /*tag= f
 FT /label= JH01 primer
 XX EP491351-A2.
 XX PD 24-JUN-1992.
 XX PF 17-DEC-1991; 91EP-0121591.
 XX PR 18-DEC-1990; 90JP-0413829.
 XX PR 11-NOV-1991; 91JP-0294464.
 XX (TAKE) TAKEDA CHEM IND LTD.

```
XX Iwasa S, Taka H, Watanabe T, Tada H;
XX WPI; 1992-209528/26.
XX P-PSDB; AAR24722.
XX Chimeric monoclonal antibodies - contain anti-human fibrin
XX antibody light and heavy chain variable and constant for treating
XX thrombotic conditions e.g. myocardial infarction
XX Example; Figure 15; 87pp; English.
XX Poly(A)+ RNA was prepd. from mouse anti-urokinase
XX antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as
XX a template, an anti-urokinase antibody VK cDNA was amplified with
XX the mc-kappa primer as primer for first strand synthesis, and the
XX 3'mv-kappa and 5'mv-kappa primers as primers for the PCR. The
XX amplified fragment was restriction digested and ligated into a
XX restriction fragment of pTB1423 to give an anti-urokinase antibody
XX VK cDNA contg. Plasmid pTB1456. The sequence of this plasmid is
XX given in AAQ25667. The cDNA is a functional VK gene. The sequence of
XX the primer (mc-gamma-1) is given in AAQ25689.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 378 BP; 92 A; 100 C; 91 G; 95 T; 0 other;
XX
Query Match 66.8%; Score 274.6; DB 13; Length 378;
Best Local Similarity 86.4%; Pred. No. 2.5e-76;
Matches 317; Conservative 0; Mismatches 44; Indels 6; Gaps 1;
QY 47 TCTGTCTCATGTGCGAGCTTCAGGAGTCGGGACCTGCTCGTGGTGAAGCCTTCTCAGTCTC 106
DB 2 TCGACTGTGAGTGGCAACTAGTGGAGTCGGGACCTGGCTGTGAACTTCTCAGTCTC 61
QY 107 TGTCCCTCACTGCATGTCTGCTGCTATCAATCACCAGTGTATGCTCGGAGCTGGA 166
DB 62 TGTCCCTCACTGCATGTCTGCTGCTATCAATCACCAGTGTATGCTCGGAGCTGGA 121
QY 167 TCGGCGAGTTTCAGGAACAACACTGGAGTGGGTGATGAGTACATAAGTACAGTGTATCA 226
DB 122 TCGGCGAGTTTCAGGAACAACACTGGAGTGGGTGATGAGTACATAAGTACAGTGTATCA 181
QY 227 CTACCTTACAAACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAAGACC 286
DB 182 CTAGTTACAAACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAAATACC 241
QY 287 AGTTCTTCTACAGTTGAATCTGTGACTACTGGGACACGTCACATATTACTGTGCAA 346
DB 242 AGTTCTTCTGAGTTGAATCTGTGACTCTGAGGACACTGCCACATATTACTGTGCAA 301
QY 347 GATCCCTAGCTGGACTACGGCT-----ATGGACTACTGGGGTCAAGGAACCTCAGTCA 400
DB 302 GATGGGTGATTTCGACGCGGGTGACTACTTTGACTACTTGGGGCCAAGGACCAAGTCA 361
QY 401 CCGTCTC 407
DB 362 CCGTCTC 368
RESULT 15
AAQ67358
ID AAQ67358 standard; DNA; 714 BP.
XX
XX AAQ67358;
XX
XX 25-MAR-2003 (updated)
XX 27-MAR-1995 (first entry)
XX
XX Anti-traseolide 02/01/01 scFv.
XX Binding protein; immobilization; chimeric protein;
XX anchoring protein; Saccharomyces cerevisiae; pUR4143;
XX musk fragrance; traseolide; polymerase chain reaction;
```

```
KW PCR; amplification; primer; light chain; hybridoma; scFv;
KW single chain antibody; monoclonal antibody; ds.
XX Synthetic.
XX WO9418330-A1.
XX
XX 18-AUG-1994.
XX
XX 10-FEB-1994; 94WO-EP00427.
XX
XX 10-FEB-1993; 93EP-0200350.
XX
XX (UNIL ) UNILEVER NV.
XX (UNIL ) UNILEVER PLC.
XX
XX De Geus P, Frenken LGJ, Klis FM, Toschka HY, Verrips CT;
XX WPI; 1994-279751/34.
XX
XX Immobilised binding proteins for specific cpds - obt'd. by
XX expressing chimeric proteins comprising the binding protein and a
XX cell wall-anchoring protein in host cells
XX
XX Disclosure; Page 35; 78pp; English.
XX
XX Valuable compounds are isolated from complex mixtures by use of
XX immobilized ligands composed of an anchoring protein and a binding
XX protein. A gene encoding such a chimeric protein that will anchor
XX in the cell wall of a lower eukaryote, e.g. S. cerevisiae, and which
XX binds traseolide with high specificity, was constructed using plasmid
XX pUR4143. This plasmid contains a gene encoding an scFv-TRAS
XX fragment of anti-traseolide antibody 02/01/01 (AAQ67358) obtained by
XX PCR amplification of hybridoma cDNA using primers AAQ67353-54 for
XX the heavy chain, and primers AAQ67355-56 for the light chain.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 714 BP; 174 A; 188 C; 178 G; 174 T; 0 other;
XX
Query Match 66.4%; Score 272.8; DB 15; Length 714;
Best Local Similarity 87.9%; Pred. No. 1.2e-75;
Matches 311; Conservative 0; Mismatches 37; Indels 6; Gaps 1;
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 5777422

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	411	100.0	411	6	AR024276	AR024276 Sequence
2	411	100.0	411	6	AR045129	AR045129 Sequence
3	411	100.0	411	6	BD011353	BD011353 Chimeric
4	411	100.0	411	6	E05354	E05354 DNA encodin
5	411	100.0	411	6	E05420	E05420 cDNA sequen
6	411	100.0	411	6	E43823	E43823 Chimeric an
7	337.4	82.1	450	10	MMIGVHR2	X05878 Mouse mRNA
8	335.4	81.6	408	10	MUSIGHDOA	L20961 Mus musculu
9	332.2	80.8	423	6	AX236250	AX236250 Sequence
10	330.2	80.3	402	10	MUSIGHQOC	L20957 Mus musculu
11	329.4	80.1	399	10	MUSIGHDOB	L20962 Mus musculu
12	327.8	79.8	417	10	MMU05284	U05284 Mus musculu
13	322	78.3	408	6	AX027688	AX027688 Sequence
14	321	78.1	1517	10	MMU65534	U65534 Mus musculu
15	319.4	77.7	825	12	SCU65536	U65536 Synthetic M
16	315	76.6	460	10	MUSIGHXX	M19894 Mouse Ig re
17	312.4	76.0	432	10	MMU291693	AJ291693 Mus muscu
18	307	74.7	485	10	MUSIGHAAC	M19899 Mouse Ig re
19	302.6	73.6	358	10	MUSOHP138G	D12726 Mus musculu
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27	291.8	71.0	351	10	MUSIGHJY	M19775 Mouse Ig ac
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ALIGNMENTS

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LOCUS AR024276
DEFINITION Sequence 30 from patent US 5795965.
ACCESSION AR024276
VERSION AR024276.1 GI:3977570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 411)
Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
Saldanha,J.William.
TITLE Reshaped human to human interleukin-6 receptor
JOURNAL Patent: US 5795965-A 30 18-AUG-1998;

411 bp DNA linear PAT 05-DEC-1998

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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
LOCUS AR045129 411 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5817790.
ACCESSION AR045129
VERSION AR045129.1 GI:5966594
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Teuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
Saldanha,J.William.
TITLE Reshaped human antibody to human interleukin-6 receptor
JOURNAL Patent: US 5817790-A 30 06-OCT-1998;
FEATURES
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Location/Qualifiers
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BASE COUNT 95 a 114 c 92 g 110 t
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LOCUS BD011353 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Chimeric antibody against human interleukin-6 receptor.
ACCESSION BD011353
VERSION BD011353.1 GI:18639726
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE
AUTHORS Teuchiya,M., Sato,K., Bendig,M.M., Jones,S.T. and Saldanha,H.W.
TITLE Chimeric antibody against human interleukin-6 receptor
JOURNAL Patent: JP 2001083151-A 27 30-MAR-2001;
CHUGAI PHARMACEUTICAL CO LTD
COMMENT
OS Mus sp. (mouse)
PN JP 2001083151-A/27
PD 30-MAR-2001
PF 28-JUL-2000 JP 2000229748
PR MASAYUKI TSUCHIYA,KO SATO,MARY MARGARET BENDIGU,PI STEVEN
TAREN JONES,
PI HOSE WILLIAM SALDANHA
PC G01N33/53,A61K38/00,A61K39/395,A61K39/395,A61P35/00,PC
G01N33/577//C07K16/28,
PC C07K19/00,C12N15/09,(C12N15/09,C12R1:91),A61K37/02,C12N15/00,
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Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
E05354
LOCUS E05354 411 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding V region of H chain of mouse monoclonal antibody against human interleukin-6 receptor.
ACCESSION E05354
VERSION E05354.1 GI:2173543
KEYWORDS JP 1993227970-A/4.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
AUTHORS Tsuchiya,M., Sato,I., Mearii,M.B., Suteilibun,T.J. and Hose,U.S.
TITLE RECONSTRUCTED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
JOURNAL Patent: JP 1993227970-A 4 07-SEP-1993;
COMMENT CHUGAI PHARMACEUT CO LTD
PN JP 1993227970-A/4
PD 07-SEP-1993
PF 19-FEB-1992 JP 1992032084
PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU, SUTEILIBUN TAREN JIYONZU, HOSE UIRAMU SARUDANA PC
C12N15/13, C07K15/06, C12N15/10, C12P21/08, C12Q1/68//C07K15/28, PC C12N5/20,
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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LOCUS E05420 411 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA sequence encoding mouse monoclonal antibody H chain against human IL-6 receptor.
ACCESSION E05420
VERSION E05420.1 GI:2173609
KEYWORDS JP 1993236966-A/27.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
AUTHORS Tsuchiya,M., Sato,I., Mearii,M.B. and Suteilibun,T.J.
TITLE DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
JOURNAL Patent: JP 1993236966-A 27 17-SEP-1993;
COMMENT CHUGAI PHARMACEUT CO LTD
OS (mouse)
PN JP 1993236966-A/27
PD 17-SEP-1993
PF 25-APR-1991 JP 1991095476
PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU, SUTEILIBUN TAREN JIYONZU
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CC hypothetical: No;
CC anti-sense: No;
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FT mat_peptide 55..411
FT /product="mouse monoclonal antibody H chain against human IL-6 receptor mature peptide".
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
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RESULT 6
LOCUS E43823 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Chimeric antibody against human interleukin-6 receptor.
ACCESSION E43823
VERSION E43823.1 GI:18627756
KEYWORDS JP 2000116391-A/27.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
AUTHORS Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
TITLE Chimeric antibody against human interleukin-6 receptor
JOURNAL Patent: JP 2000116391-A 27 25-APR-2000;
CHUGAI PHARMACEUT CO LTD
COMMENT OS Mus sp. (mouse)
PN JP 2000116391-A/27
PD 25-APR-2000
PF 29-NOV-1999 JP 1999338286
PR PI MASAYUKI TSUCHIYA, ISAO SATO, BENDIGU MARY MARGARET, PI JONES
STEVEN TAREN,
PI SARUDANA HOSE WILLIAM
PC C12N15/09,C07K16/18,C07K16/26,C07K19/00,C12N5/10,C12P21/08, PC
C12N15/00,
CC C12N5/00
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Best Local Similarity 100.0%; Pred. No. 4.7e-128;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
LOCUS MMIGVHR2 450 bp mRNA linear ROD 07-MAY-1992
DEFINITION Mouse mRNA for immunoglobulin heavy chain variable region.
ACCESSION X05878 Y00330
VERSION X05878.1 GI:52526
KEYWORDS constant region; Ig heavy chain; variable region.
SOURCE Mus musculus (house mouse)
ORGANISM Mus-musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 450)
AUTHORS Grant,F.J., Levin,S.D., Gilbert,T. and Kindsvogel,W.
TITLE Improved RNA sequencing method to determine immunoglobulin mRNA
sequence
JOURNAL Nucleic Acids Res. 15 (13), 5496 (1987)
MEDLINE 87260030
PUBMED 3601683
REFERENCE 2 (bases 1 to 450)
AUTHORS Grant,F.J.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1987) Dr. Francis Grant, Zymogenetics, Inc., 2121
North 35th Street, Seattle, Wa 98103, USA
FEATURES Location/Qualifiers
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Matches 365; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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RESULT 8
MUSIGHDQA
LOCUS Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.
DEFINITION L20961
ACCESSION L20961.1 GI:309344
VERSION V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain;
KEYWORDS monoclonal antibody; processed gene.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.
Structural profile of idiotype, anti-idiotype and
anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
system
Eur. J. Immunol. 24 (11), 2874-2881 (1994)

JOURNAL
MEDLINE 95045941
PUBMED 7957578

REFERENCE 2 (bases 1 to 408)
Iwasaki, Y., Takabatake, H., Monestier, M. and Ferrone, S.
Idiotypic diversity and variable region gene usage by mouse
anti-HLA-DQ3 mAb
Immunogenetics 42 (2), 90-100 (1995)

JOURNAL
MEDLINE 95331832
PUBMED 7607710

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Matches 377; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

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Qy 181 GGAACAACTGGAGTGGATGGGTACATAAGTTACAGTGTGTATCACTACTCAACACCCA 240
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Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCA 411
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RESULT 9
AX236250
LOCUS AX236250
DEFINITION Sequence 108 from Patent WO0164749.
ACCESSION AX236250
VERSION AX236250.1 GI:15795925
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kloetzer, W.S. and Hanna, N.
Method for preparing anti-mif antibodies
Patent: WO 0164749-A 108 07-SEP-2001;
Idex Pharmaceuticals Corporation (US)

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BASE COUNT
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Qy	121	ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGGATCCGGCAGTTTCCA	180
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Qy	181	GGAAACAAACTGGAGTGGATGGGCTACATAAGTTTACAGTGGTATCATCTACTACAACCCA	240
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Qy	301	TTGAATTTCTGTGACTACTGGGGACACGCTCCACATATTTACTGTGCAAGA---TCCCTTAGC	356
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Qy	357	TCGGACTACGGCTA--TGGACTACTGGGTCAAGGAACCTTCAGTCAACGTCCTCTCTCA	411
Db	361	TATCACGTGGGCTACTTTTGACTCTGTGGGGCAAGGCCACCACTCTCAACGTCCTCTCTCA	417

RESULT 10	MUSIGHDQC
Locus	Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.
DEFINITION	402 bp linear mRNA ROD 04-JUN-1996
ACCESSION	L20957
VERSION	L20957.1 GI:309348
KEYWORDS	V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 402) Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S. TITLE Structural profile of idiotype, anti-idiotypic and anti-anti-idiotypic monoclonal antibodies in the HLA-DQ3 antigenic system Eur. J. Immunol. 24 (11), 2874-2881 (1994) JOURNAL MEDLINE 95045941 PUBMED 7957578 REFERENCE 2 (bases 1 to 402) AUTHORS Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S. TITLE Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb Immunogenetics 42 (2), 90-100 (1995) JOURNAL MEDLINE 95331832 PUBMED 7607710

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Db	301	TTGAATTCCTGACTACTGGAGACAGCCACATATTACTGTCAAGTTCTATGAT---	357	
Qy	361	ACTACGGCTATGACTACTGGGTCAGGAACCTCAGTCAACCGTCTCTCTCA	411	
Db	358	-----GGCTTTGACTACTGGGCCAAGGCACCACTCTCACAGTCTCTCTCA	402	
RESULT 11				
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LOCUS	MUSIGHDB 399 bp mRNA linear ROD 04-JUN-1996			
DEFINITION	Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.			
ACCESSION	L20962			
VERSION	L20962.1 GI:309346			
KEYWORDS	V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 399)			
AUTHORS	Iwasaki.Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.			
TITLE	Structural profile of idiotype, anti-idiotypic and anti-anti-idiotypic monoclonal antibodies in the HLA-DQ3 antigenic system			
JOURNAL	Eur. J. Immunol. 24 (11), 2874-2881 (1994)			
MEDLINE	95045941			
PubMed	7957578			

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REFERENCE 2 (bases 1 to 399)
AUTHORS Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S.
TITLE Idiotypic diversity and variable region gene usage by mouse
anti-HLA-DQ3 mAb
JOURNAL Immunogenetics 42 (2), 90-100 (1995)
MEDLINE 95331832
PUBMED 7607710
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MMU05284
LOCUS Mus musculus BALB/c/J immunoglobulin heavy chain complete variable
region (Igh) mRNA, partial cds.
U05284
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VERSION U05284.1 GI:463457
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Tempest,P.R., White,P., Buttle,M., Carr,F.J. and Harris,W.J.
TITLE Identification of framework residues required to restore antigen
binding during reshaping of a monoclonal antibody against the
glycoprotein gB of human cytomegalovirus
JOURNAL Int. J. Biol. Macromol. 17 (1), 37-42 (1995)
MEDLINE 95290446
PUBMED 7772562
REFERENCE 2 (bases 1 to 417)
AUTHORS Tempest,P.R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1994) Philip R. Tempest, ICOS Corporation, 22021
20th Ave SE, Bothell, WA 98021, USA
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Matches 369; Conservative 0; Mismatches 42; Indels 6; Gaps 1;
Qy 1 ATGAGAGTGGCTGATTCTTTTGTGGCTGTTTCACAGCCTTTCTCGGTATCTCTGTCTGTGATGTG 60
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Db 361 ACT 363
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RESULT 13
AX027688
LOCUS
DEFINITION Sequence 5 from Patent WO0043774.
ACCESSION AX027688
VERSION AX027688.1 GI:10189558
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eszhar,Z. and Willner,I.
TITLE Detection of small molecules by use of a piezoelectric sensor
JOURNAL Patent: WO 0043774-A 5 27-JUL-2000;
YISSUM RES DEV CO (IL); ESHAR ZELIG (IL); WILLNER ITAMAR (IL);
YEDA RES & DEV (IL)
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ORIGIN

Query Match 78.3%; Score 322; DB 6; Length 408;
Best Local Similarity 90.7%; Pred. No. 8.4e-98;
Matches 343; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTCGGTATCTCTGTCGATGTG 60
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RESULT 14
MMU65534
LOCUS
DEFINITION Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.
1517 bp mRNA linear ROD 28-AUG-1996
MMU65534
Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.

ACCESSION U65534
VERSION U65534.1 GI:1513181
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Full-length immunoglobulin gamma chain
JOURNAL Unpublished
REFERENCE
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal
Parade, Parkville, Victoria 3052, Australia
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CDS

BASE COUNT 373 a 445 c 358 g 341 t
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Query Match 78.1%; Score 321; DB 10; Length 1517;
Best Local Similarity 95.7%; Pred. No. 2.1e-97;
Matches 330; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTCGGTATCTCTGTCGATGTG 60
Db 44 ATGAGAGTCTGATCTTTTGGCTGTTTCACAGCCTTTCTCGGTATCTCTGTCGATGTG 103
Qy 61 GAGCTTCAGGAGTCGGGACCTCTCTGTTGAGCCTTCTCAGTCTCTGTCCTCCTCCTGC 120
Db 104 GAGCTTCAGGAGTCGGGACCTCTGTTGAGCCTTCTCAGTCTCTGTCCTCCTCCTGC 163
Qy 121 ACTGTCACTGGCTACTCAATCACTACAGTGATCATGCTGGAGCTGGAGCTCGGAGTTTCCA 180
Db 164 ACTGTCACTGGCTACTCAGTCACAGTCAATATATGCTGGAACTGGATCCGCGAGTTTCCA 223
Qy 181 GAAACAAACTCGAGTGGGTACATAAGTTACAGTGGTATCAGTCTCCTCCTCCTCCTCA 240
Db 224 GAAACAAACTCGAGTGGGTACATAAGTTACAGTGGTATCAGTCTCCTCCTCCTCCTCA 283
Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACAGTCTCTCTCTACAG 300
Db 284 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACAGTCTCTCTCTCGAG 343
Qy 301 TTGAATTCCTGACTACTGGGACACGTCACATATTACTGTGCA 345
Db 344 TTGAATTCCTGACTACTGGGACACGTCACATATTACTGTGCA 388

RESULT 15
SCU65536
LOCUS
DEFINITION Synthetic Mus musculus single chain Fv antibody precursor mRNA, complete cds.
825 bp mRNA linear SYN 07-MAR-2000
SCU65536
Synthetic Mus musculus single chain Fv antibody precursor mRNA, complete cds.

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ACCESSION U65536 GI:1513185
VERSION U65536.1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 825)
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Single chain Fv with signal sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 825)
AUTHORS Xiao,X.W. and Frenkel,M.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) Biomedical Engineering, CSIRO, 343 Royal
Parade, Parkville, Victoria 3052, Australia
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            VSLGDSQVSISSRSSQSIHNSNGNTYLEWYKPGQSPKLLIYKVSNRFSGVDRFSGS
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BASE COUNT 201 a 201 c 200 g 223 t
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Best Local Similarity 95.4%; Pred. No. 6.9e-97;
Matches 329; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 ATGAGAGTCGATCTTTTGGCTGTTCACAGCCTTCTCGTATCCTGTCGTGATGTG 60
Db 13 ATGAGAGTCGATCTTTTGGCTGTTCACAGCCTTCTCGTATCCTGTCGTGATGTG 72
Qy 61 CAGCTTCAGGAGTCGGGACCTGCTCGTGAAGCTTCTCAGTCTCTGTCCTCACCTGC 120
Db 73 CAGCTTCAGGAGTCGGGACCTGCGGCTGTGTGAACCTTCTCAGTCTCTGTCCTCACCTGC 132
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTCATCGCTGAGCTGGATCCGGCAGTTTCCA 180

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Db 133 ACTGTCACTGGGCTACTCAGTCACCACTGAATATGCTCGGAATGGATCCGGCAGTTTCCA 192
Qy 181 GGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCAGTCTACAAACCCA 240
Db 193 GGAAACAAACTGGAGTGGGCTGGGCTACATAAACTACAGTGGTAGCACTAGCTACAAACCCA 252
Qy 241 TCTCTCAAAAGTCGAATCTCTATCAGTCTCGAGACACATCCAAAGAACAGTTCTTCTCTACAG 300
Db 253 TCTCTCAAAAGTCGAATCTCTATCAGTCTCGAGACACATCCAAAGAACAGTTCTTCTCTGAG 312
Qy 301 TTGAATCTGTGACTACTGGGACACGTCACATATTTACTGTGCA 345
Db 313 TTGAATCTGTGACTACTGAGGACAGCCACATATTTACTGTGCA 357

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Job time : 1643.91 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 02:40:25 ; Search time 1521.59 Seconds
(without alignments)
10243.574 Million cell updates/sec

Title: US-09-114-285A-28
Perfect score: 381
Sequence: 1 ATGGTGTCCTCAGTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb ba.*
- 2: gb htg.*
- 3: gb in.*
- 4: gb in.*
- 5: gb ov.*
- 6: gb pat.*
- 7: gb ph.*
- 8: gb pl.*
- 9: gb pr.*
- 10: gb ro.*
- 11: gb sts.*
- 12: gb sy.*
- 13: gb un.*
- 14: gb vi.*
- 15: em ba.*
- 16: em fun.*
- 17: em hum.*
- 18: em in.*
- 19: em mu.*
- 20: em om.*
- 21: em or.*
- 22: em ov.*
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- 28: em un.*
- 29: em vi.*
- 30: em htg hum.*
- 31: em htg inv.*
- 32: em htg other.*
- 33: em htg mus.*
- 34: em htg pin.*
- 35: em htg rod.*
- 36: em htg mam.*
- 37: em htg vrt.*
- 38: em sy.*
- 39: em htgo hum.*
- 40: em htgo mus.*
- 41: em htgo other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	100.0	381	6	AR024275 Sequence
2	381	100.0	381	6	AR045128 Sequence
3	381	100.0	381	6	BD011352 Chimeric
4	381	100.0	381	6	E05353 DNA encodin
5	381	100.0	381	6	E43822 Chimeric an
6	381	100.0	381	6	E05419 cDNA sequen
7	359.2	94.3	381	10	S0261 Ig VL=anti-
8	359.2	94.3	381	6	I33380 Sequence 1
9	359.2	94.3	381	10	MUSIVJR
10	357.6	93.9	381	10	MUSIGRAAL
11	356	93.4	381	10	MMU16689
12	355.2	93.2	378	10	AF045496
13	351.2	92.2	381	6	AR016717 Sequence
14	351.2	92.2	381	10	MMU05217
15	351.2	92.2	381	10	AF466770
16	349.8	91.8	378	10	MUSIGK527A
17	349.6	91.8	959	10	BC015292
18	348.6	91.5	381	6	A51499
19	348.6	91.5	381	6	AR085777 Sequence
20	346.4	90.9	381	6	AR024279 Sequence
21	346.4	90.9	381	6	AR045132 Sequence
22	346.4	90.9	381	6	BD011356 Chimeric
23	346.4	90.9	381	6	E05357 DNA encodin
24	346.4	90.9	381	6	E43826 Chimeric an
25	346.4	90.9	381	6	E05423 cDNA sequen
26	341.2	89.6	366	10	MUSIGCKO
27	338.4	88.8	382	6	AR301133 Sequence
28	337	88.5	399	10	AY081858
29	332.6	87.3	372	6	E06647
30	330	86.6	345	10	MUSIGKCPW
31	328.8	86.3	395	10	MUSIGKAAAM
32	324	85.0	1019	10	BC027418
33	322.4	84.6	408	6	AR067477
34	322.4	84.6	408	6	AR032023
35	322.4	84.6	408	6	AR038519 Sequence
36	322.4	84.6	408	6	AR267246
37	322.4	84.6	408	6	E05888
38	322.4	84.6	408	10	S63022
39	320.8	84.2	408	6	AR050865
40	320.8	84.2	408	6	AR219876
41	320.8	84.2	408	6	E07922
42	312	81.9	324	10	MMIGKL229
43	312	81.9	324	10	MMIGKL233
44	312	81.9	324	10	MMIGKL38
45	312	81.9	324	10	MUSIGKAVD

ALIGNMENTS

RESULT 1	AR024275	Sequence 28 from patent US 5795965.	381 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR024275	Sequence 28 from patent US 5795965.				
DEFINITION	Sequence 28 from patent US 5795965.					
ACCESSION	AR024275					
VERSION	AR024275.1	GI:3977569				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 381)					
AUTHORS	Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.William.					
TITLE	Reshaped human to human interleukin-6 receptor					
JOURNAL	Patent: US 5795965-A 28 18-AUG-1998;					

Db 61 GATATCCAGATGACACAGACTACATCTCCCTGTCTGCCTCTCTGGGACAGAGTCACC 120

 Q_Y

221 ATCAGTTGAGGGCAAGTCAGGACATTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180

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Qy      181 GATGAACATTTAAACTCTGTACTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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Db      241 AGGTTTCAGTGGCAGTGGGTCTCGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
Qy      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
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Qy      361 GGGACCAAGCTGGAATAAAT 381
Db      361 GGGACCAAGCTGGAATAAAT 381

RESULT 6
E05419
LOCUS      E05419      387 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION cDNA sequence encoding mouse monoclonal antibody kappa type L chain
            variable region against human IL-6 receptor.
ACCESSION E05419
VERSION   E05419.1 GI:2173608
KEYWORDS  JP 1993236966-A/26.
SOURCE    Mus musculus
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 387)
AUTHORS   Tsuchiya,M., Sato,I., Mearii,M.B. and Suteibun,T.J.
TITLE     DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY
          TO HUMAN INTERLEUKIN-6 RECEPTOR
JOURNAL   Patent: JP 1993236966-A 26 17-SEP-1993;
          CHUGAI PHARMACEUT CO LTD
COMMENT   OS (mouse)
          PN JP 1993236966-A/26
          PD 17-SEP-1993
          PF 25-APR-1991 JP 1991095476
          PI TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU,
          SUTEIBUN TAREN JIYOONZU
          PC C12N15/13//C12P21/08;
          CC strandedness: Double;
          CC topology: Linear;
          CC hypothetical: No;
          CC anti-sense: No;
          CC *source: deposit=MCIMB40366;
          CC *source: cell_lines=PM1;
          CC *source: clone=ppm-k3;
          FH Key
          FH Location/Qualifiers
          FT sig_peptide 1..60
          FT mat_peptide 61..387
          FT L chain
          FT variable region against human IL-6 receptor
          FT mature peptide'.
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BASE COUNT 106 a 87 g 98 t
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Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
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Qy      61 GATATCCAGATGACACAGACTACATCTCCCTCTGTCTGCTCTCTGGGAGACAGAGTCAACC 120
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Qy      121 ATCAGTTGCGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Db      121 ATCAGTTGCGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
Qy      181 GATGAACATTTAAACTCTGTACTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
Db      181 GATGAACATTTAAACTCTGTACTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
Qy      241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAAACAACCTGGAGCAA 300
Db      241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAAACAACCTGGAGCAA 300
Qy      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
Db      301 GAAGACATTTGCCACTTACTTTTCCCAACAGGGTAAACAGCTTCCGTACACAGTTTCGGAGGG 360
Qy      361 GGGACCAAGCTGGAATAAAT 381
Db      361 GGGACCAAGCTGGAATAAAT 381

RESULT 7
S50261
LOCUS      S50261      381 bp      mRNA      linear      ROD 08-MAY-1993
DEFINITION Ig VL-anti-CD4 mAb M-T151 variable region light chain {J2, chimeric
            antibody} [mice, hybridoma cells, mRNA Partial, 381 nt].
ACCESSION S50261
VERSION   S50261.1 GI:260761
KEYWORDS  Mus sp.
SOURCE    Mus sp.
ORGANISM  Mus sp.
REFERENCE 1 (bases 1 to 381)
AUTHORS   Weissenhorn,W., Scheuer,W., Kaluza,B., Schwirzke,M., Reiter,C.,
          Flieger,D., Lenz,H., Weiss,E.H., Rieber,E.P., Riehmuller,G. et.al.
          Combinatorial functions of two chimeric antibodies directed to
          human CD4 and one directed to the alpha-chain of the human
          interleukin-2 receptor
JOURNAL   Gene 121 (2), 271-278 (1992)
MEDLINE   93077041
PUBMED    1446824
REMARK    GenBank staff at the National Library of Medicine created this
          entry [NCBI gibseq 119499] from the original journal article.
          This sequence comes from Fig. 1a.
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BASE COUNT 105 a 92 c 83 g 101 t
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ORIGIN
Query Match          94.3%; Score 359.2; DB 10; Length 381;
Best Local Similarity 96.6%; Pred. No. 1.1e-106;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTGCTCTGTTTCAAGGTACAGATGT 60
Db 1 ATGATGCTCCTGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACAGATGT 60

Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGCTCTGCTCTCTGGAGACAGAGTCAACC 120
Db 61 GATATCCAGATGACACAGACTATATCTCCCTCTCTGCTCTCTGGAGACAGAGTCAACC 120

Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATAGCAGTTATTAACTGGTATCATCAGCAAAACCA 180
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Qy 181 GATGGAATTAATACTCTGATCTATACATCAAGATTACACTCAGGAGTCCCATCA 240
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Qy 241 AGTTTCAGTGCAGTGGTCTGGAACAGATTATTCTCTCACCATTAAACCTGGAGCA 300
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Qy 301 GAAGACATTCGACTTACTTTTGGCAACAGGGTAACACGTTCCGTACACGTTCCGAGGG 360
Db 301 GAAGATGTTGCACCTTACTTTTGGCAACAGGGTAATAGCTTCGTACACGTTCCGAGGG 360

Qy 361 GGGACCAAGCTGGAATAAA 380
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 8
133380
LOCUS          133380          393 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION     Sequence 1 from patent US 5591629.
ACCESSION      I33380
VERSION        I33380.1  GI:1824171
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 393)
AUTHORS        Rodriguez,M. and Miller,D.J.
TITLE          Monoclonal antibodies which promote central nervous system
               remyelination
JOURNAL        Patent: US 5591629-A 1 07-JAN-1997;
FEATURES       Location/Qualifiers
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               1..393
               /organism="unknown"
BASE COUNT     105 a 96 c 89 g 103 t
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Query Match          94.3%; Score 359.2; DB 6; Length 393;
Best Local Similarity 96.6%; Pred. No. 1.1e-106;
Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACAGATGT 60
Db 1 ATGATGCTCCTGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACAGATGT 60

Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGCTCTGCTCTCTGGAGACAGAGTCAACC 120
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Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAGCAGTTATTAACTGGTATCATCAGCAAAACCA 180
Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAGCAGTTATTATTAACTGGTATCATCAGCAAAACCA 180

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Db 181 GATGGAATTAATACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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Db 241 AGTTTCAGTGCAGTGGTCTGGAACAGATTATTCTCTCACCATTAAACCTGGAGGG 360

Qy 301 GAAGACATTCGACTTACTTTTGGCAACAGGGTAACACGTTCCGTACACGTTCCGAGGG 360
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Qy 361 GGGACCAAGCTGGAATAAA 380
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 9
MUSIVJR
LOCUS          393 bp      mRNA      linear      ROD 25-MAY-1995
DEFINITION     Mus musculus germline immunoglobulin light chain variable region
               and joining region mRNA, 5' end.
ACCESSION      L35316.1  GI:829182
VERSION        L35316.1  GI:829182
KEYWORDS       germline; immunoglobulin light chain; joining region; variable
               region.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
               1 (bases 1 to 393)
REFERENCE      1 (bases 1 to 393)
AUTHORS        Miller,D.J. and Rodriguez,M.
TITLE          A monoclonal autoantibody that promotes central nervous system
               remyelination in a model of multiple sclerosis is a natural
               autoantibody encoded by germline immunoglobulin genes
JOURNAL        J. Immunol. 154 (5), 2460-2469 (1995)
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               /db_xref="GI:829183"
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Matches 367; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTTTCAAGGTACAGATGT 60
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Qy 61 GATATCCAGATGACACAGACTACATCTCCCTGCTCTGCTCTCTGGAGACAGAGTCAACC 120
Db 61 GATATCCAGATGACACAGACTATATCTCCCTCTCTGCTCTCTGGAGACAGAGTCAACC 120

Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAGCAGTTATTAACTGGTATCATCAGCAAAACCA 180
Db 121 ATCAGTTGCGAGGCAAGTCAGGACATTAAGCAGTTATTATTAACTGGTATCATCAGCAAAACCA 180

Qy 181 GATGGAATTAATACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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sig_peptide 1. .60
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V_region 61. .381
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misc_feature 61. .324
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J_segment 346. .381
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BASE COUNT 105 a 92 c 83 g 101 t
ORIGIN

Query Match 93.4%; Score 356; DB 10; Length 381;
Best Local Similarity 96.1%; Pred. No. 1.2e-105;
Matches 365; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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DB 1 ATGATGTCCTCTGCTCAGTCTCTGGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGT 60
QY 61 GATATCCAGATGACACAGACTACATCTCTGCTCTGCTCTCTGGGAGACAGAGTCACC 120
DB 61 GATATCCAGATGACACAGACTACATCTCTGCTCTGCTCTCTGGGAGACAGAGTCACC 120
QY 121 ATCATGTCAGGGCAAGTCAGACATTTAGCAGTTATTTAACTGGTATCAGCAAAACCA 180
DB 121 ATCATGTCAGGGCAAGTCAGACATTTAGCAGTTATTTAACTGGTATCAGCAAAACCA 180
QY 181 GATGGAATTTAACTCTGATCTACACATCAGATTACACTCAGGAGTCCCATCA 240
DB 181 GATGGAATTTAACTCTGATCTACACATCAGATTACACTCAGGAGTCCCATCA 240
QY 241 AGGTTTCAGTGGCAGTGGTCTGGAACAGATTATTTCTCACCATTAACTGGAGCAA 300
DB 241 AGGTTTCAGTGGCAGTGGTCTGGAACAGATTATTTCTCACCATTAGCACTGGAACAA 300
QY 301 GAAGACATTCACCTACTTTTGGCAACAGGGTAACACGTTCCGTACAGTTCGGAGGG 360
DB 301 GAAGATATTGCCACTTACTTTTGGCAACAGGGTAATACGTTCCGTGACGTTCCGGTGA 360
QY 361 GGGACCAAGCTGGAAATAAA 380
DB 361 GGCACCAAGCTGGAAATAAA 380

RESULT 12
LOCUS AF045496 378 bp mRNA linear ROD 28-FEB-1998
DEFINITION Mus musculus dc7 anti-poly(dC) monoclonal antibody kappa light chain variable region, (Igk) mRNA, partial cds.
ACCESSION AF045496
VERSION AF045496.1 GI:2906075
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 378)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 378)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA

FEATURES
source 1. .378
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/chromosome="6"
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/cell_line="spleen cell hybridoma"
gene <1. .>378
/gene="Igk"
CDS 1. .>378
/gene="Igk"
/codon_start=1
/product="anti-poly(dC) monoclonal antibody kappa light chain"
/protein_id="AAC04524.1"
/db_xref="GI:2906076"
/translation="MSSAQLFLGLLLCFQGRCDIQMTQTSSLSASLGRVITISCR A
ATVFCQGNLTLPYFGGKLEIK"

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/gene="Igk"
V_region 58. .342
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J_segment 343. .>378
/gene="Igk"

BASE COUNT 99 a 93 c 88 g 98 t
ORIGIN

Query Match 93.2%; Score 355.2; DB 10; Length 378;
Best Local Similarity 96.5%; Pred. No. 2.2e-105;
Matches 363; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 5 TGTCTCTCAGTCAGTCTCTGGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGTGATA 64
DB 2 TGTCTCTCTGCTCAGTCTCTGGTCTCTGTTGCTCTGTTTCAAGGTACCAGATGTGATA 61
QY 65 TCCAGATGACACAGACTACATCTCTGCTCTGCTCTCTGGGAGACAGAGTCACCATCA 124
DB 62 TCCAGATGACGAGACTCCATCTCTGCTCTGCTCTCTGGGAGACAGAGTCACCATCA 121
QY 125 GTTTCAGGGCAAGTCAGGACATTAGCAGTTATTTAACTGGTATCAGCAGAAACCATG 184
DB 122 GTTTCAGGGCAGTCAGGACATTAGCAATTTATTTAACTGGTATCAGCAGAAACCATG 181
QY 185 GAACTATTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGT 244
DB 182 GAACTGTATAACTCTGCTCTACTACACATCAAGATTGCACTCAGGAGTCCCATCAAGGG 241
QY 245 TCAGTGGCAGTGGTCTGGAACAGATTATTTCTCACCATTAACTGAGCAAGAAG 304
DB 242 TCAGTGGCAGTGGTCTGGAACAGATTATTTCTCACCATTAGCACTGAGCAAGAAG 301
QY 305 ACATTGCCACTTACTTTTGGCAACAGGGTAACACGTTCCGTACACGTTCCGAGGGGGGA 364
DB 302 ATATTGCCACTTACTTTTGGCAACAGGGTAATACGTTCCGTACACGTTCCGAGGGGGGA 361
QY 365 CCAAGCTGGAAATAAA 380
DB 362 CCAAGCTGGAAATAAA 377

RESULT 13
LOCUS AR016717 381 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5777085.
ACCESSION AR016717

Submitted (09-JAN-2002) Department of Biological Sciences,
University of Ulsan, Ulsan 680-749, Korea

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 02:25:30 ; Search time 189.538 Seconds
(without alignments)
5426.282 Million cell updates/sec

Title: US-09-114-285a-28
Perfect score: 381
Sequence: 1 ATGGTGCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description
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2	359.2	94.3	381	14	AAQ36607
3	359.2	94.3	393	16	AAQ05311
4	351.2	92.2	381	14	AAQ45662
5	351.2	92.2	381	19	AAV36741
6	349.6	91.8	381	18	AAV59500
7	349.6	91.8	381	19	AAV34426
8	348.6	91.5	381	17	AAT35050

9	348	91.3	444	11	AAQ08608	ME4 Light Chain V
10	348	91.3	444	18	AAT43440	MAB ME4 light chain
11	348	91.3	444	20	AAV71158	Coding strand for
12	348	91.3	444	25	ABX79238	DNA encoding mouse
13	343.2	90.1	381	13	AAQ30759	p146-k3. Syntheti
14	338.4	88.8	382	18	AAT73611	CDNA encoding high
15	333.6	87.6	402	12	AAQ12061	Sequence encoding
16	333.6	87.6	402	12	AAQ12017	Sequence encoding
17	332.6	87.3	372	15	AAQ56067	Human IL-1 chimeri
18	322.4	84.6	408	21	AAQ51004	Murine immunoglob
19	320.8	84.2	408	20	AAQ99481	pKM641 LA2 immunog
20	319.2	83.8	408	14	AAQ37058	Rat immunoglobulin
21	319.2	83.8	408	15	AAQ45438	KM641 H chain vari
22	309.6	81.3	382	18	AAT73656	CDNA for humanised
23	304.8	80.0	382	18	AAT73652	CDNA for humanised
24	302.4	79.4	321	25	ABT14041	Ganglioside-associ
25	301.6	79.2	382	18	AAT73631	CDNA for humanised
26	301.6	79.2	382	18	AAT73647	CDNA for humanised
27	300	78.7	382	18	AAT73644	CDNA for humanised
28	299.2	78.5	324	16	AAT05313	B-cell lymphoma CH
29	298.2	78.3	1931	25	ABV73341	CD19-zeta chimeric
30	296	77.7	321	19	AAV07641	anti-CD22 monoclon
31	295.2	77.5	1668	22	AAQ89071	Activating polypep
32	295.2	77.5	1898	22	AAQ89073	Activating polypep
33	295.2	77.5	1734	22	AAQ89072	Activating polypep
34	295.2	77.5	2115	22	AAQ89088	MLV envelope glyco
35	294.4	77.3	324	21	AAQ27323	Murine consensus 1
36	292.2	76.7	702	22	AAC91015	Chimeric 4H6 anti-
37	292.2	76.7	702	22	AAC91016	Chimeric 4H6 anti-
38	289.8	76.1	1943	24	ABK13467	DNA encoding immun
39	289.6	76.0	324	21	AAQ01185	Murine monoclonal
40	289.6	76.0	324	21	AAQ39345	Murine anti-integr
41	288.2	75.6	913	15	AAQ81076	Bispecific CD3-L6F
42	288	75.6	1803	21	AAQ58773	DNA encoding an im
43	288	75.6	1944	25	ABX14413	DNA encoding recom
44	287.2	75.4	2023	25	ABZ75116	Anti-human seminal
45	287.2	75.4	2952	24	ABK13464	DNA encoding immun

ALIGNMENTS

RESULT 1
AAQ30755
ID AAQ30755 standard; cDNA; 381 BP.

XX AC AAQ30755;
XX DT 25-MAR-2003 (updated)
DT 30-MAR-1993 (first entry)
DE pPM-k3.
XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
KW plasmid; pPM-k3; pPM-h1; ss.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..381
FT /*tag= b

XX PN WO9219759-A1.
XX PD 12-NOV-1992.
XX PF 24-APR-1992; 92WO-JP00544.
XX PR 25-APR-1991; 91JP-0095476.
PR 19-FEB-1992; 92JP-0032084.

[illegible]

KW graft versus host disease; ulcerative colitis; sequelae;
KW myocardial infarction; mouse; murine; monoclonal; treatment; ss.
XX

OS Mus spp.

XX Key Location/Qualifiers
XX mat_peptide 1..381
FT /*tag= a

XX WO9702290-A1.

XX 23-JAN-1997.

XX 01-JUL-1996; 96WO-JP01820.

XX 17-MAY-1996; 96US-0649100.

XX 30-JUN-1995; 95JP-0188480.

XX (MOCH) MOCHIDA PHARM CO LTD.

PA (OSAB-) OSAKA BIOSCIENCE INST.

XX Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;

XX WPI; 1997-108917/10.

DR P-PSDB; AAW11815.

XX Antibody reactive with Fas ligand capable of inducing apoptosis -
PT used for diagnostic assay of Fas ligand in body fluids and for
PT treatment of diseases in which Fas ligand/Fas antigen is involved

XX Disclosure; Fig 10; 164pp; Japanese.

XX The present sequence encodes the light chain of the mouse
CC anti-apoptosis inducing human Fas ligand, monoclonal antibody,
CC F919. The antibody can be used in a Fas ligand assay, e.g. an
CC enzyme linked immunosorbent assay, to diagnose diseases in which
CC the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
CC B/C, human immunodeficiency virus, graft/host disorders,
CC ulcerative colitis or sequelae of myocardial infarction. The
CC antibody may also be used to treat such diseases.

XX Sequence 381 BP; 102 A; 94 C; 85 G; 100 T; 0 other;

Query Match 91.8%; Score 349.6; DB 18; Length 381;

Best Local Similarity 95.0%; Pred. No. 5.7e-99;

Matches 361; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGTCTCAGTCTCCTTGGTCTCTCTGTTGCTCTGTTTCAAGTACAGATGT 60

Db 1 ATGATGTCTCTGCTCAGTCTCCTTGGTCTCTGTTGCTCTGTTTCAAGTACAGATGT 60

Qy 61 GATATCCAGATGACACAGACTACATCTCCTGCTGCTCTCTGTTGCTCTGTTTCAAGTACAGATCACC 120

Db 61 GATATCCAGATGACACAGACTACATCTCCTGCTGCTCTCTGTTGCTCTGTTTCAAGTACAGATCACC 120

Qy 121 ATCAGTTGCGGGCAAGTCAGGACATTAGCAGTTATTTAACTGTTATCAGCAGAAACCA 180

Db 121 ATCAGTTGCGGGCCAGTCAGGACATTAGCAGTTATTTAACTGTTATCAGCAGAAACCA 180

Qy 181 GATGGAATATTAACTCTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240

Db 181 GATGGAATGTTAACTCTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240

Qy 241 AGGTTTCAGTGGCAGTGGTCTGGACAGATTATTTCTCACCATTACACCTGGACAA 300

Db 241 AGGTTTCAGTGGCAGTGGTCTGGACAGAAATTTCTCTCACCATTAGCAACCTGGACAA 300

Qy 301 GAACACATTGCGACTTACTTTTGGCAACAGGTAACAGCTTCGGTACAGTTTCGGAGGG 360

Db 301 GGAGATATTGCCACTTACTTTTGGCAACAGGTAAGTACGTTTCGGTGGAGTTTCGGTGGGA 360

Qy 361 GGGACCAAGCTGGAAATAAA 380

Db 361 GGGACCAAGCTGGAAATAAA 380

Db 361 GGCACCAAGCTGGAAATCAA 380

RESULT 7

AAV34426

ID AAV34426 standard; CDNA; 381 BP.

XX AAV34426;

XX 11-SEP-1998 (first entry)

XX Mouse antibody F919-9-18 light chain encoding CDNA.

XX Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
KW heart failure; kidney failure; graft-versus-host disease; antibody;
KW myocardial infarction; ischemic restenosis; endotoxic shock; ss.

OS Mus sp.

XX Key Location/Qualifiers

XX CDS 1..381

FT /*tag= a

FT /product= "F919-9-18 light chain"

FT /note= "the stop codon is not indicated"

XX WO9818487-A1.

XX 07-MAY-1998.

XX 31-OCT-1997; 97WO-JP03978.

XX 26-SEP-1997; 97JP-0262521.

XX 31-OCT-1996; 96JP-0290459.

XX 27-DEC-1996; 96JP-0351718.

XX (MOCH) MOCHIDA PHARM CO LTD.

PA (OSAB-) OSAKA BIOSCIENCE INST.

XX Nagata S, Suda T, Yatomi T;

XX WPI; 1998-271925/24.

DR P-PSDB; AAW60033.

XX Use of Fas antagonist for treatment and prevention of

PT apoptosis-related diseases - such as heart or kidney failure,

PT graft-versus-host disease or liver disease

XX Disclosure; Fig 1; 86pp; Japanese.

XX This cDNA encodes the light chain of the mouse antibody F919-9-18. This
CC is used for generating a mouse anti-human Fas ligand monoclonal antibody.
CC The invention provides the use of Fas antagonist as an agent for the
CC treatment and prevention of apoptosis-related diseases. The Fas
CC antagonist can be a partial Fas antigen peptide containing the
CC extracellular part of the protein, but lacking the signal sequence, an
CC anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is
CC preferably a humanised antibody. The Fas antagonist is used in the
CC treatment and prevention of diseases such as myocardial infarction, heart
CC failure, ischemic heart disease, acute kidney failure, graft-versus-host
CC disease, ischemic restenosis of the heart, liver or kidney, and
CC endotoxic shock, and also as an organ preservative in transplantation.
CC The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
CC system.

XX Sequence 381 BP; 102 A; 94 C; 85 G; 100 T; 0 other;

Query Match 91.8%; Score 349.6; DB 19; Length 381;

Best Local Similarity 95.0%; Pred. No. 5.7e-99;

Matches 361; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ATGTTGCTCCTCAGTCTCAGTCTCCTTGGTCTCTGTTGCTCTGTTTCAAGTACAGATGT 60

Db 1 ATGATGTCTCTGCTCAGTCTCCTTGGTCTCTGTTGCTCTGTTTCAAGTACAGATGT 60

QY 61 GATATCCAGATGACACAGACTACATCTCCCTGCTGCTCTCTCTGGGAGACAGAGTCACC 120
 DB 61 GATATCCAGATGACACAGACTACATCTCCCTGCTGCTCTCTCTGGGAGACAGAGTCACC 120
 QY 121 ATCAGTTGCGGGCAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180
 DB 121 ATCAGTTGCGGGCAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180
 QY 181 GATGAACTATTAACTCTGATCTACTACACATCAAGATTACATCTCAGGAGTCCCATCA 240
 DB 181 GATGAACTATTAACTCTGATCTACTACACATCAAGATTACATCTCAGGAGTCCCATCA 240
 QY 241 AGTTTCAGTGGCAGTGGGCTGGACAGATTATCTCTCACCATTAACTGAGGAGCAA 300
 DB 241 AGTTTCAGTGGCAGTGGGCTGGGCAAAATTTATCTCACCATTAGCAACCTGGAAACA 300
 QY 301 GAAGACATTTGCCACTTACTTTTGGCCAAAGGGTAAACAGCTTCCGTACACAGTTCCGAGGG 360
 DB 301 GGAGATATTGCCACTTACTTTTGGCCAAAGGGTAGTACGCTTCCGTGACGTTCCGTTGGA 360
 QY 361 GGGACCAAGCTGGAAATAAA 380
 DB 361 GGCACCAAGCTGGAAATCAA 380

RESULT 8

AAT35050
 ID AAT35050 standard; cDNA; 381 BP.
 XX
 AC AAT35050;
 DT 10-JAN-1997 (first entry)
 XX
 DE MAB VL17E6 light chain (specific for human alphav integrins).
 KW Monoclonal antibody; MAb; integrin; cell-matrix interaction;
 KW tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
 KW imaging; detection; radiolabel; ss.
 XX
 OS Mus musculus.

Key Location/Qualifiers

FT sig_peptide 1..60
 FT mat_peptide /*tag= a
 FT mat_peptide 61..381
 FT mat_peptide /*tag= b
 XX
 PN EP719859-A1.
 XX
 PD 03-JUL-1996.
 XX
 PF 06-DEC-1995; 95EP-0119233.
 XX
 PR 20-DEC-1994; 94EP-0120165.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;
 PI Rosell E;
 XX
 DR WPI: 1996-302345/31.
 DR P-PSDB; AAR99003.
 XX
 PT New human integrin V chain-specific monoclonal antibody - and
 PT related DNA and hybridomas, for treatment and diagnostic imaging of
 PT tumours, esp melanoma.
 XX
 PS Claim 14; Figure 17a; 54pp; English.
 XX
 CC A monoclonal antibody which reacts only with the alphav chain of
 CC human alphav integrins; which blocks attachment of alphav integrin
 CC bearing cells to integrin substrate; which reverses established cell

CC matrix interactions caused by alphav integrin; which blocks tumour
 CC development and which has no cytotoxic activity, may be used to
 CC treat tumours, especially melanoma (but also glioma, carcinoma)
 CC optionally coupled to a cytokine such as interleukin-2. The
 CC monoclonal antibody may also be used for diagnostic imaging of
 CC tumours and assessment of tumour growth when conjugated to a
 CC radiolabel or a radio opaque-agent.

SQ Sequence 381 BP; 105 A; 88 C; 85 G; 103 T; 0 other;

Query Match 91.5%; Score 348.6; DB 17; Length 381;
 Best Local Similarity 95.0%; Pred. No. 1.2e-98;
 Matches 360; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGTTGCTCTCAGTCTCAGTTCCCTTGGTCTCTCTGCTCTGTTTCAAGGTACCAGATGT 60
 DB 1 ATGTTGCTCTCAGTCTCAGTTCCCTTGGTCTCTCTGCTCTGTTTCAAGGTACCAGATGT 60
 QY 61 GATATCCAGATGACACAGACTACATCTCCTCTGCTCTCTCTGGGAGACAGAGTCACC 120
 DB 61 GATATCCAGATGACACAGACTACATCTCCTCTGCTCTCTCTGGGAGACAGAGTCATC 120
 QY 121 ATCAGTTGCGGGCAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180
 DB 121 ATCAGTTGCGGGCAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180
 QY 181 GATGAACTATTAACTCTGATCTACTACACATCAAGATTACATCTCAGGAGTCCCATCA 240
 DB 181 GATGAACTATTAACTCTGATCTACTACACATCAAGATTACATCTCAGGAGTCCCATCA 240
 QY 241 AGTTTCAGTGGCAGTGGGCTGGAAACAGATTATTTCTCACCATTAACTGAGGAGCAA 300
 DB 241 AGTTTCAGTGGCAGTGGGCTGGAAACAGATTATTTCTCACCATTAGTAACCTGGAGCAA 300
 QY 301 GAAGACATTTGCCACTTACTTTTGGCCAAAGGGTAAACAGCTTCCGTACACAGTTCCGAGGG 360
 DB 301 GAAGATATTGCCACTTACTTTTGGCCAAAGGGTAAACAGTTTCCGTACACAGTTCCGAGGG 360
 QY 361 GGGACCAAGCTGGAAATAAA 379
 DB 361 GGGACCAAGCTGGAAATGA 379

RESULT 9

AAQ08608
 ID AAQ08608 standard; DNA; 444 BP.

XX AAQ08608;

AC AAQ08608;

XX 25-MAR-2003 (updated)

DT 04-MAR-1993 (first entry)

XX ME4 Light Chain V Region (mouse).

XX Monoclonal antibody; chimera; light; heavy; chain; constant;

XX variable; antigen; diagnosis; cancer; tumour; ss.

XX Mus musculus.

OS Mus musculus.

XX Key

XX Location/Qualifiers

XX 61..444

XX /*tag= a

XX WO9002569-A.

XX 22-MAR-1990.

XX 06-SEP-1989; 89WO-US03852.

XX 06-SEP-1988; 88US-0240624.

XX 08-SEP-1988; 88US-0241744.

XX 13-SEP-1988; 88US-0243739.

XX 04-OCT-1988; 88US-0253002.

QY 181 GATGGAACATTAATACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
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 Db 181 GATGGAACATGTTAACTCTGATCTACGATACATCAAGATTACACTCAGGAGTCCCATCA 240
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 QY 241 AGGTTTCAGTGGCAGTGGGTCTCGAACAAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
 |||||
 Db 241 AGGTTTCAGTGGCAGTGGGTCTCGAACAAGATTATTTCTCACCATTAGCAACCTGGAGCAA 300
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 QY 301 GAAGACATTCGCACCTACTCTTTTGGCAACAAGGTAACAGCTTCCGTACACGTTTCGGAGGG 360
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 Db 301 GAAGATATTGCCAGTTACTTTTGGCAACAAGGTTATAGCCCTCCGTGAGACGTTCCGTGGA 360
 |||||
 QY 361 GGGACCAAGCTGGAATAAA 380
 |||||
 Db 361 GGGACCAAGTTGGAAATCAA 380
 |||||

RESULT 14

AAT73611

ID AAT73611 standard; cDNA; 382 BP.

XX AC AAT73611;

XX DT 19-DEC-1997 (first entry)

XX DE cDNA encoding light chain variable region of KM1259 antibody.

XX

KW Complementarity determining region; CDR; light chain; treatment;
 KW variable region; murine; mouse; human; interleukin 5; IL-5;
 KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;
 KW assay; diagnosis; allergic respiratory disease;
 KW chronic bronchitis; ds.

XX OS Mus spp.

XX

XX FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT mat_peptide /*tag= a
 FT 61..381
 FT /*tag= b

XX PN WO9710354-A1.

XX PD 20-MAR-1997.

XX PF 11-SEP-1996; 96WO-JP02588.

XX PR 11-SEP-1995; 95JP-0232384.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Anazawa H, Furuya A, Hanai N, Tida A, Koike M;

XX PI Nakamura K, Takatsu K;

XX DR WPI: 1997-202249/18.

XX DR P-PSDB; AAW21844.

PT Antibody against alpha-chain of human interleukin 5 receptor -

PT useful for diagnosis and treatment of respiratory allergic diseases,

PT e.g. chronic bronchitis

XX

XX PS Example 2; Pages 122-123; 238pp; Japanese.

XX

CC The present sequence encodes the light chain variable region of the
 CC murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
 CC monoclonal antibody (MAB) KM1259. KM1259 is produced by the hybridoma
 CC FERM BP-5134, which was prepared by immunising Balb/c mice with
 CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
 CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAB
 CC can be used to detect or assay for hIL-5R alpha and cells
 CC expressing it on their surface, especially to diagnose allergic
 CC respiratory diseases, e.g. chronic bronchitis. It can also be used

CC to treat such diseases.

XX SQ Sequence 382 BP; 102 A; 89 C; 90 G; 101 T; 0 other;
 Query Match 88.8%; Score 338.4; DB 18; Length 382;
 Best Local Similarity 93.2%; Pred. No. 1.8e-95;
 Matches 354; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 ATGCTGTCTTCAGCTCAGTTCCCTGGTCTCTCTGCTCTGTTTTCAGGTTACAGATGT 60
 |||||
 Db 1 ATGATGTCTCTGCTCAGTTCCCTGGTCTCTCTGTTTTCAGGATATCAGATGT 60
 |||||
 QY 61 GATATCCAGATGACACAGACTACATCTCCTGCTCTCTCTGCGAGACAGAGTCAAC 120
 |||||
 Db 61 GATATCCAGATGACACAGGCTACATCTCCTGCTCTCTCTGCGAGACAGAGTCAAC 120
 |||||
 QY 121 ATCAGTTTCAGGGCAAGTCAGGACATTAGCAGTTATTTAACTGGTATCAGCAAAACCA 180
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 QY 181 GATGGAACATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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 QY 241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAAACAACCTGGAGCAA 300
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 QY 361 GGGACCAAGCTGGAATAAA 380
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 Db 361 GGGACCAAGTTGGAAATAAA 380
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RESULT 15

AAQ12061

ID AAQ12061 standard; DNA; 402 BP.

XX AC AAQ12061;

XX DT 25-MAR-2003 (updated)

XX DT 15-AUG-1991 (first entry)

XX

XX DE Sequence encoding light (kappa) chain variable region of murine
 XX DE IC11 immunoglobulin.
 XX KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.

XX OS Mus musculus.

XX

XX FH Key Location/Qualifiers
 FT CDS 22..402
 FT /*tag= a
 FT /product= mouse MAB 1C11 L(kappa)-chain
 FT variable region

XX PN WO9107493-A.

XX PD 30-MAY-1991.

XX PF 13-NOV-1990; 90WO-US06615.

XX PR 13-NOV-1989; 89US-0433730.

XX PA (XOMA) XOMA CORP.

XX PA (GREG) GREEN CROSS CORP.

XX PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX DR WPI: 1991-178105/24.

Search completed: October 24, 2003, 03:57:07
Job time : 191.538 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:39:05 ; Search time 1673.61 Seconds
(without alignments)
5532.953 Million cell updates/sec

Title: US-09-114-285A-28

Perfect score: 381

Sequence: 1 ATGTGTCCTAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	339.4	89.1	1459	13	BQ918407
2	338.6	88.9	827	12	BF152061
3	336.8	88.4	669	10	BF123422
4	327.2	85.9	830	12	BF455041

ALIGNMENTS

RESULT 1

BQ918407

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ918407. 1459 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8885602 NCI CGAP Co24 Mus musculus cDNA clone
IMAGE:6397382 5', mRNA sequence.

BQ918407 GI:22333105

EST.

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

1 (bases 1 to 1459)

NTM-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AMI3895 row: c column: 15

High quality sequence start: 165

BI103114 602889345
BF580940 602100636
BF578083 602094759
BF582283 602101109
BF123744 601760491
BY235531 BY235531
BF581992 602099448
AZ313441 1M0016K06
BG963548 602831226
CB958057 AGENCOURT
BO881840 AGENCOURT
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AW405753 UI-HF-BL0
CB956317 AGENCOURT
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BM914405 AGENCOURT
CB986236 AGENCOURT
CB984807 AGENCOURT
AW406886 UI-HF-BL0
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AW406323 UI-HF-BL0
CB957697 AGENCOURT
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322.4 84.6 708 12 BI103114
312 81.9 725 10 BF580940
7 309.8 81.3 966 10 BF578083
8 300.8 81.0 626 10 BF582283
9 300.4 78.8 774 10 BF123744
10 235.6 77.6 354 13 BY235531
11 294.8 77.4 772 10 BF581992
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13 250.4 65.7 714 12 BG963548
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18 240.8 63.2 554 14 CB956317
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20 240.8 63.2 1019 12 BM914405
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45 236 61.9 738 14 CB987788

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

708 bp mRNA linear EST 26-JUN-2001
114 Mus musculus cdna clone IMAGE:5044690

RESULT 6			
BF580940			
LOCUS	BF580940	725 bp	linear
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RESULT 7
BF578083
LOCUS
DEFINITION 602094759p1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209015 5',
            mRNA sequence.
ACCESSION BF578083
VERSION BF578083.1 GI:11651795
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 966)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9774 row: e column: 16
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            Average insert size 1.6 kb. Constructed by Life
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BASE COUNT 277 a 276 c 205 g 208 t
ORIGIN
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Best Local Similarity 92.3%; Pred. No. 8.9e-85;
Matches 348; Conservative 0; Mismatches 27; Indels 2; Gaps 2;
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Db |||||
Qy 53 TATCCAGATGACACAGTACATCTCCCTGCTGCTCTGCGAGACAGTCCCAT 122
Db |||||
Qy 72 TATCCAGATGACACAGTACATCTCCCTGCTGCTCTGCGAGACAGTCCCAT 131
Db |||||
Qy 123 CAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACAGA 182
Db |||||
Qy 132 CAGTTGACGGTCAAGTCAGGACATTAGCAATTATTAACTGGTATCAGCAGAAACCGGA 191
Db |||||
Qy 183 TGGAACTATTAACTCCTGATCTACTACATCATCAAGATTATCACTCAGGAGTCCCATCAAG 242
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Qy 243 GTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTACCATTAACAACCTGGAGCAGA 302
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Qy 252 GTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTACCATTAACAACCTGGAGCAGA 311
Db |||||
Qy 303 AGACATTGCCACTTACTTTTGCACAGGGTAACACGCTTCGATACAGTTTCGAGGGGG 362
Db |||||
Qy 312 AGATA-TGCCACTTAC-TTTCGCAACAGGTAACCTTACCTTCCGTTGGACGTTGGTGGAG 369
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Qy 363 GACCAAGCTGGAATAAA 379
Db |||||
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Db 370 CACCAAGGTGGAAGTCA 386
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BF582283
LOCUS
DEFINITION 602101109f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224267 5',
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ACCESSION BF582283
VERSION BF582283.1 GI:11655995
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9814 row: a column: 04
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Location/Qualifiers
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            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 178 a 153 c 137 g 158 t
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Matches 342; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
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Qy 1 ATGATGTCCTCTGCTCAGTTCCTGGTCTCTGCTGCTGTTTCAAGGTACCATGTGT 59
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Qy 61 GATATCCAGATGACACAGACTACATCTCCTGCTCTCTCTCTGGAGACAGAGTCAAC 120
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Qy 60 GATATCCAGATGACACAGACTACATCTCCTGCTCTCTCTCTGGAGACAGAGTCAAC 119
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Qy 180 GATGGAATGTTTAACTCCTGATCTATTACATCAATTTTACATTCAGGAGTCCCATCA 239
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Qy 240 AGGTTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATCAGCAACCTGGAACT 299
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Qy 301 GAAGACATTCGCATTTACTTTTGCACAGGGTAACACGCTTCGTCGTACACGTTTCGGAGGG 360
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Qy 300 GAAGATATTGCCACTTACTATTGTCAGCAGTATTTTAAAGCTTCCATTGACGCTCGGCTCG 359
Db |||||
```


Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.usc.riken.co.jp>) for further details.

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/mor_cfp=man
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Technologies Note, this is a NCI CGAP

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BASE COUNT	216 a	204 c	175 g	176 t	1 others
ORIGIN					

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Best Local Similarity 89.3%; Pred. NO. 3.6e-80;
Matches 317; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 86 CTTCCCTGTCCTCTCTGGAGACAGAGTCCACATCAGTTGCAGTGGAGAGTCAGGGCA 143

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		TTAGCAGTTATTATAACTGGTATCAGCAGAAACCGATGGAATCTGTAAAATCCTGATCT	205
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Qy	206	ACTACATCAAGATTACACTCAGGAGTCCCATCAAGTTTCAGTGGCAGTGGGTCTGGA	265
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QY	266	CAGATTATTCTCTCACCATTAAACACCTGGAGCAAGACATTTGCACCTTACTTTTGGC	325
DB	264	CAGATTATTCTCTCAGCATCTCCGACACCTGGACCTGAGCATATNCCGCTTACTATTTC	323

264 CAGATATATCTCTCCACATCCAGACATCGGACCTGGAGATATTCACATCATATG
 326 AACAGGGTTAACAGCTTCCGTCACAGTTCCGAGGGGGACCAAGCTCGAAATAAA 380
 Qy

Db 324 AGCAGTATCGTTACCTTCGCGTGGACGTTCCGTTGGAGGCCACCAAGTTGGAAATCAA 378

	GSS 29-SEP-2000
	DNA linear
LOCUS	730 bp
DEFINITION	Mouse 10kb plasmid UCGM1 library musculus genomic
ACCESSION	U0016K06 F, genomic survey sequence.
	clone UCGC1M0016K06
	clone UCGC1M0016K06
	clone UCGC1M0016K06

ACCESSION AZ313441
VERSION AZ313441.1 GI:10358341

VERSION AZ313441.1 GI:10358341
KEYWORDS GSS.

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)

SOURCE ORGANISM	REFERENCE
Mus musculus	Metazoa: Chordata
Mus musculus	Metazoa: Chordata
Mus musculus	Metazoa: Chordata

Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia

REFERENCE
Mammalia; Eutheria; Rodentia
1 (bases 1 to 730)

REFERENCE
1 (bases 1 to 730)
Dunn, D., Aoyagi, A., Barber

AUTHORS
Dunn, D.; Aoyagi, A.; Barber
Islam, H.; Longacre, S.; Mah

ISLAM, H.; LONGACRE, S.; STONE, M.; ROSE, M.; ROSE, R.; STONE and WRIGHT D. Weiss R.

TITLE Mouse whole genome scaffold

TITLE	Mouse whole genome scaffold
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100	100

plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: K column: 06
 Seq primer: CTTGTGTAACACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 730.
 Location/Qualifiers
 1. 730

FEATURES source

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 /db_xref="taxon:10090"
 /clone="JUGC1M0016K06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 212 a 146 c 160 g 212 t

BASE COUNT ORIGIN

Query Match 68.8%; Score 262.2; DB 28; Length 730;
 Best Local Similarity 90.9%; Pred. No. 4.6e-70;
 Matches 279; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 44 TTCAAGGTACAGATGTGATATCCAGATGACACAGACTATCTCCCTGTCCTC 103
 Db 702 TCCTAGGTACAGATGATATCCAGATGACACAGACTATCTCCCTGTCCTC 643

QY 104 TCGGAGACAGTCCACATCAGTTCAGGCGAGTCAGGACATTAGCAGTATTTAACT 163
 Db 642 TGGGAGACAGTCCACATCAGTTCAGGCGAGTCAGGACATTAGCAGTATTTAACT 583

QY 164 GGTATCAGCAGAAACACAGATGGAACCTATTAACTCCTGATCTACTACACATCAAGATTAC 223
 Db 582 GGTATCAGCAGAAACACAGATGGAACCTATTAACTCCTGATCTACTACACATCAAGATTAC 523

QY 224 ACTCAGGAGTCCATCAAGGTTAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCACA 283
 Db 522 ACTCAGGAGTCCATCAAGGTTAGTGGCAGTGGGTCTGGGAGGAGATTATTTCTCACA 463

QY 284 TTAACAACCTGGAGAGACATTGCCACTTACTTTTGCCAAACAGGGTAACAGCTTC 343
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QY 344 CGTACAC 350

Db 402 CTCACAC 396

RESULT 13 BG963548 LOCUS

DEFINITION 602831226F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4985791 5',
 714 bp mRNA linear EST 12-JUN-2001
 mRNA sequence.
 ACCESSION BG963548
 VERSION BG963548.1 GI:14351185
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 714)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LIAM10994 row: c column: 08
 High quality sequence stop: 712.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:10090"
 /clone="IMAGE:4985791"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 189 a 178 c 167 g 180 t

FEATURES source

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 Best Local Similarity 78.7%; Pred. No. 2.1e-66;
 Matches 299; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1 ATGTGTCTCAGCTCAGTTCCTTGGTCTCTGTTGCTCTGTTTTCAGGTACCAGATGT 60
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QY 61 GATATCAGATGACACAGACTACATCTCTGCTGCTCTCTGGGAGACAGAGTACC 120
 Db 76 GACCTCAGATGATTCAGTCTCCATCGTCCATGTTTGCCTCTCTGGGAGACAGTGTCA 135

QY 121 ATCAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTTAACTGGTATCAGCAGAAACCA 180
 Db 136 CTCTCTTGTGCGACTAGTCAGGGCATTTAGAGTTAATTTAGACTGGTATCAGCAGAAACCA 195

QY 181 GATGGAATTTAACTCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
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QY 241 AGGTTTCACTGTCAGTGGGTCTGGAAACAGATTATTTCTCTCACCATTAACAACCTGGAGCAA 300
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QY 301 GAAGACATTGCCACTTACTTTTGGCAACAGGGTAACAGCTTCCGTCACACGTTTCGGAGGG 360
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Qy 361 GGGACCAAGCTGGAATAAA 380
Db 376 GGGACCAAGCTGGAATAAA 395

RESULT 14
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LOCUS AGENCOURT 13785358 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30351230 5', mRNA sequence.
CB958057
ACCESSION CB958057.1 GI:30214174
VERSION CB958057.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 558.
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/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatgcc); Site_2: SfiI (ggccgcttcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 199 a 210 c 196 g 156 t 1 others
ORIGIN
Query Match 63.6%; Score 242.4; DB 14; Length 762;
Best Local Similarity 77.4%; Pred. No. 6.5e-64;
Matches 294; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 ATGGTGCTCAGCTCAGTTCCTGGTCTCGTGTCTCTGTTTCAAGGTACCAGATGT 60
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Db 99 GACATCCAGATGACCCAGTCTCCATCTCTCTCTGCTGCTATCTGTAGGAGACAGATCTCC 158
Qy 121 ATCAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTTAACTGGTATCAGCAAAACCA 180
Db 159 ATCACTTGCCGGCAAGTCAGGACATTATCAGTATTAAATGGTATCAGCAAAACCA 218

Qy 181 GATGGAACCTATTAACTCTCTGATCTACTACATCAAGATTACTACTCAGGAGTCCCATCA 240
Db 219 GGGAAAGCCCTAAACTCTCTGATCTACTACTCCTCACTTTGCAAGGTGGAGTCCCATCA 278
Qy 241 AGGTTTCAGTGGCAGTGGTCTGGAACAGATTATTTCTCTCACCATTACACCTGGGACAA 300
Db 279 AGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCCTCTCACCATCAGCAGTCTGCAACCT 338
Qy 301 GAAGACATTGCCACTTACTTTTCCCAACAGGTAACACGCTTCGGTACACGTTTCGGAGGG 360
Db 339 GAAGATTTCGCAACTTACTACTGTGACGAGAGTACAGAAACCGTTCCTCTTCGCGCGGA 398
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 399 GGGACCAAGCTGGAATCAA 418

RESULT 15
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5', mRNA sequence.
ACCESSION BQ881840
VERSION BQ881840.1 GI:22273848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2502 row: g column: 22
High quality sequence stop: 655.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6295725"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 212 a 274 c 200 g 202 t
ORIGIN
Query Match 63.6%; Score 242.4; DB 13; Length 888;
Best Local Similarity 77.4%; Pred. No. 7e-64;
Matches 294; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 ATGGTGCTCAGCTCAGTTCCTGGTCTCGTGTCTGTTTCAAGGTACCAGATGT 60
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Qy 61 GATATCCAGATGACACAGACTACATCTCTCCCTGCTGCTCTCTGGGAGACAGAGTCA 120

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Db 76 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 135
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Qy 241 AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTTCTCACCATTAAACCTGGAGCAA 300
Db 256 CGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGACTGCAGCCT 315
Qy 301 GAAGACATTGCCACTTACTTTTGCCAAACAGGGTAACAGCTTCCGTACACGTTGGAGGG 360
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Db 376 GGGACCAAGTGGATATCAA 395

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Job time : 1680.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:51:21 ; Search time 53.8788 Seconds
(without alignments)
3121.209 Million cell updates/sec

Title: US-09-114-285A-28

Perfect score: 381

Sequence: 1 ATGCTGTCCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	381	100.0	381	1	US-08-436-717-28
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4	359.2	94.3	393	5	PCT-US95-05262-1
5	351.2	92.2	381	1	US-08-458-516-4
6	348.6	91.5	381	2	US-08-574-699A-1
7	346.4	90.9	381	1	US-08-137-117D-36
8	346.4	90.9	381	1	US-08-436-717-36
9	338.4	88.8	382	3	US-08-836-561-28
10	338.4	88.8	382	4	US-09-434-132-28
11	322.4	84.6	408	1	US-08-408-133-5
12	322.4	84.6	408	1	US-08-454-683-5
13	322.4	84.6	408	2	US-08-454-680-5
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18	320.8	84.2	408	2	US-08-483-528B-19
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21	309.6	81.3	382	3	US-08-836-561-102
22	309.6	81.3	382	4	US-09-434-122-102
23	304.8	80.0	382	3	US-08-836-561-97
24	304.8	80.0	382	4	US-09-434-122-97
25	301.6	79.2	382	3	US-08-836-561-70
26	301.6	79.2	382	3	US-08-836-561-91
27	301.6	79.2	382	4	US-09-434-122-70

Sequence 91, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 3, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 6, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-137-117D-28
; Sequence 28, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid

RESULT 7
US-08-137-117D-36
Sequence 36, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
* APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SAIDANHA, Jose

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2003, 03:57:16 ; Search time 904.875 Seconds
(without alignments)
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Title: US-09-114-285A-28
Perfect score: 381
Sequence: 1 ATGCTGTCCTCAGCTCAGTT.....GGACCAAGCTGGAATAAAT 381

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359.2	94.3	393	8	US-08-779-784-20
2	359.2	94.3	393	12	Sequence 20, Appl
3	351.2	92.2	381	12	Sequence 63, Appl
4	349.6	91.8	381	14	Sequence 4, Appl
5	338.4	88.8	382	14	Sequence 1, Appl
6	332.4	84.6	408	9	Sequence 28, Appl
7	322.4	84.6	408	12	Sequence 9, Appl
8	322.4	84.6	408	14	Sequence 9, Appl
9	320.8	84.2	408	14	Sequence 9, Appl
10	309.6	81.3	382	14	Sequence 102, Appl
11	304.8	80.0	382	14	Sequence 97, Appl
12	301.6	79.2	382	14	Sequence 70, Appl
13	301.6	79.2	382	14	Sequence 91, Appl
14	300	78.7	382	14	Sequence 87, Appl
15	299.2	78.5	324	8	Sequence 22, Appl
16	294.4	77.3	324	13	Sequence 3, Appl

17	291.2	76.4	321	12	US-10-310-674A-33
18	289.6	76.0	324	9	Sequence 33, Appl
19	289.6	76.0	324	14	Sequence 72, Appl
20	288.2	75.6	916	9	Sequence 6, Appl
21	288.2	75.6	1527	14	Sequence 29, Appl
22	288	75.6	1803	10	Sequence 347, Appl
23	276	72.4	285	8	Sequence 2, Appl
24	262.2	68.8	315	14	Sequence 23, Appl
25	260.8	68.5	321	11	Sequence 30, Appl
26	257.6	67.6	324	14	Sequence 9, Appl
27	256.4	67.3	306	14	Sequence 3, Appl
28	254	66.7	324	14	Sequence 28, Appl
29	252	66.1	435	9	Sequence 13, Appl
30	250.4	65.7	402	8	Sequence 1, Appl
31	250.4	65.7	402	8	Sequence 5, Appl
32	250.4	65.7	402	12	Sequence 5, Appl
33	247.2	64.9	407	10	Sequence 27, Appl
34	245.4	64.4	307	14	Sequence 9, Appl
35	243	63.8	708	12	Sequence 3, Appl
36	242.4	63.6	974	10	Sequence 29, Appl
37	239.2	62.8	390	12	Sequence 10, Appl
38	239.2	62.8	714	14	Sequence 18, Appl
39	239.2	62.8	729	12	Sequence 125, App
40	239.2	62.8	729	14	Sequence 125, App
C 41	237.2	62.3	520	10	Sequence 1210, Ap
C 42	237.2	62.3	520	13	Sequence 1210, Ap
C 43	237.2	62.3	520	14	Sequence 1210, Ap
44	236	61.9	387	9	Sequence 1, Appl
45	234.4	61.5	387	9	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-779-784-20
; Sequence 20, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:

Db 121 ATCGGTTGGGACAAAGTGAGGACATTTATCAATATTTTAACTGGTATCGGAAGAAACCA 180
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Db 181 GATGGAATTTGTTGAACTCTGATCTACCAACATCAAGATTACACTCAGGAGTCCCATCA 240
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Db 241 AGGTTTCAGTGGCAGGCTCGGAACAGATTATTTCTCACCATTAGTACCTCGAGGCAA 300
Qy 301 GAAGACATTTGCCACTTACTTTTGGCAACAGGTTAAACGCTTCCGTACACGTTGGAGGG 360
Db 301 GAAGATATTTGCCACTTACTTTTGGCAACAGGTTTATACGTTCCGTACACGTTGGAGGG 360
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 361 GGGACCAAGTTGGAATAAA 380

RESULT 6
US-09-764-304-9
; Sequence 9, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(408)
; NAME/KEY: mat_peptide
; LOCATION: (85)..(408)
; NAME/KEY: sig_peptide
; LOCATION: (25)..(84)
US-09-764-304-9

Query Match 84.6%; Score 322.4; DB 9; Length 408;
Best Local Similarity 90.5%; Pred. No. 3.5e-98;
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 1 ATGGTGCTCCTCAGCTCAGTTCCTCGTCTCCTGTTGCTGTTTCAAGGTACCAGATGT 60
Db 25 ATGATGCTCTGCTCAGTTCCTCGTCTCCTGTTGCTGTTTCAAGGTACCAGATGT 84
Qy 61 GATATCCAGATCACACAGACTACATCCCTGCTCTGCTCTCTCGGAGACAGAGTCAACC 120

Db 85 GATATCCAGATGACACAGACTGATCTCCTCGCTGCTCTCTGGGAGACAGAGTCAACC 144
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Qy 241 AGGTTTCAGTGGCAGTGGGCTCGGAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300
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Qy 301 GAACACATTCGCCTTACTTTTGGCAACAGGTTAAACGCTTCCGTACACGTTGGAGGG 360
Db 325 GAAGATATTTGCCACTTACTTTTGTACATAGTATAGTAACTTCCGTGAGCGTTGGTGA 384
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 385 GGCACCAAGCTGGAATAAA 404

RESULT 7
US-10-166-626-9
; Sequence 9, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(408)
; NAME/KEY: mat_peptide
; LOCATION: (85)..(408)
; NAME/KEY: sig_peptide
; LOCATION: (25)..(84)
US-10-166-626-9

Query Match 84.6%; Score 322.4; DB 12; Length 408;
Best Local Similarity 90.5%; Pred. No. 3.5e-98;
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 1 ATGGTGCTCCTCAGCTCAGTTCCTGTTGCTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 60

Db 25 ATGATGCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 84
Qy 61 GATATCCAGATGACACACACTACATCTCCCTGCTCTCTGCGGAGACAGAGTCAAC 120
Db 85 GATATCCAGATGACACACACTGCAATCTCCCTGCTCTCTGCGGAGACAGAGTCAAC 144
Qy 121 ATCAGTTGCGGGCAAGTACAGACATTAGCAGTATTATTTAACTGGTATCAGCAAAACCA 180
Db 145 ATCAGTTGCGGGCAAGTACAGACATTAGTAAATTTAACTGGTATCAGCAAAACCA 204
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Db 205 GATGGAACCTGTTAACTCCTGATCTTTTACTCATCAAAATTTACACTCGGGAGTCCCATCA 264
Qy 241 AGGTTCACTGGCGAGTGGGTCTGGAACAGATTATTTCTCACCATTTAACTCGGAGCAA 300
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Qy 301 GAAGACATTCGCACCTTACTTTTGGCAACAGGGTAACACGTTCCGTATCACGTTCCGGAGGG 360
Db 325 GAAGATATTCGCACCTTACTTTTGTGTCATCAGTATAGTAACTTCCGTGGAGCTTCGGTGGA 384
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 385 GGCACCAAGCTGGAATACAA 404

RESULT 8

US-10-265-713-9
; Sequence 9, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US/07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
; NAME/KEY: CDS
; LOCATION: (25)..(408)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(408)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (25)..(84)
US-10-265-713-9

Query Match 84.6%; Score 322.4; DB 14; Length 408;
Best Local Similarity 90.5%; Pred. No. 3.5e-96;
Matches 344; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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Db 25 ATGATGCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTCAAGGTACCAGATGT 84
Qy 61 GATATCCAGATGACACACACTACATCTCCCTGCTCTCTGCGGAGACAGAGTCAAC 120
Db 85 GATATCCAGATGACACACACTGCAATCTCCCTGCTCTCTGCGGAGACAGAGTCAAC 144
Qy 121 ATCAGTTGCGGGCAAGTACAGACATTAGCAGTATTATTTAACTGGTATCAGCAAAACCA 180
Db 145 ATCAGTTGCGGGCAAGTACAGACATTAGTAAATTTAACTGGTATCAGCAAAACCA 204
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Qy 241 AGGTTCACTGGCGAGTGGGTCTGGAACAGATTATTTCTCACCATTTAACTCGGAGCAA 300
Db 265 AGGTTCACTGGCGAGTGGGTCTGGAACAGATTATTTCTCACCATCAGCAACTCGGAGCT 324
Qy 301 GAAGACATTCGCACCTTACTTTTGGCAACAGGGTAACACGTTCCGTATCACGTTCCGGAGGG 360
Db 325 GAAGATATTCGCACCTTACTTTTGTGTCATCAGTATAGTAACTTCCGTGGAGCTTCGGTGGA 384
Qy 361 GGGACCAAGCTGGAATAAA 380
Db 385 GGCACCAAGCTGGAATACAA 404

RESULT 9

US-10-195-752-19
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; KOIKE, MASAMICHI
; SHITARA, KENYA
; HANAI, NOBUO
; KUWANA, YOSHIOHISA
; HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/195,752
; FILING DATE: 16-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-195-752-19

Query Match 84.2%; Score 320.8; DB 14; Length 408;
Best Local Similarity 90.3%; Pred. No. 1.2e-97;
Matches 343; Conservative 0; Mismatches 37; Indels 0; Gaps 0;


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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICANT: US/08/836,561
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: JP 232384/95
;   FILING DATE: 11-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Lawrence, III, Stanton T
;     REGISTRATION NUMBER: 25,736
;     REFERENCE/DOCKET NUMBER: 7005-115-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 212-790-9090
;     TELEFAX: 212-869-9741
;     TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 97:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 382 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: Other
;     SEQUENCE DESCRIPTION: SEQ ID NO: 97:
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; US-10-283-349-97
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; Query Match      80.0%; Score 304.8; DB 14; Length 382;
; Best Local Similarity 87.6%; Pred. No. 2.9e-92;
; Matches 333; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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; DB      1  ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTGCTCTCTGTTTCAAGATATCAGATGT 60
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; QY      61  GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCTCTCTGGGAGACAGAGTCACC 120
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; QY      121  ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGATTATTAACTCGGTATCAGCAGAAACCA 180
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; QY      181  GATGGAACTATTAAACTCCTGATCTACTACATCAGATTACACTCAGGAGTCCCATCA 240
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; QY      241  AGGTTACGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACATTAAACAACCTCGAGCAA 300
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; QY      301  GAAGACATTGCCACTTACTTTTGGCCAAACAGGTAACACGTTCCGTACACGTTCCGAGGG 360
; DB      301  GAAGATTTTGCCACTTACTTTTGGCCAAACAGGTTATACGTTCCGTACACGTTCCGCGCA 360
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; QY      361  GGGACCAAGCTGGAAATAAA 380
; DB      361  GGGACCAAGTGGAAATAAA 380
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; RESULT 12
; US-10-283-349-70
;   Sequence 70, Application US/10283349
;   Publication No. US20030096977A1
;   GENERAL INFORMATION:
;     APPLICANT: KOIKE, Masamichi
;     FURUYA, Akio
;     NAKAMURA, Kazuyasu
;     IIDA, Akihiro
;     ANAZAWA, Hideharu
;     HANAI, No. US20030096977A1uo
;     TAKATSU, Kiyoshi
;   TITLE OF INVENTION: Antibody Against Human Interleukin-5
;     Receptor Alpha Chain
;   NUMBER OF SEQUENCES: 106
;   CORRESPONDENCE ADDRESS:

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GenCore version 5.1.6
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(without alignments)
352.133 Million cell updates/sec

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Perfect score: 661
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107863

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
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3	627	94.9	127 14	AA28670
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9	621	93.9	128 24	AA28670

10	619	93.6	127	14	AA28670	Mouse C4G1 Ig light
11	619	93.6	127	17	AA28670	Variable region of
12	606	91.7	127	17	AA28670	MAB VL17E6 light c
13	599	90.6	127	13	AA28670	p146-k3 protein pr
14	590	89.3	126	12	AA28670	Mouse MAB 1C11 L c
15	590	89.3	127	12	AA28670	Light (kappa) chai
16	587	88.8	124	15	AA28670	Human/murine IL-1
17	574	86.8	128	21	AA28670	Murine immunoglobulin
18	574	86.8	128	22	AA28670	Ganglioside GD3 sp
19	574	86.8	128	24	AA28670	Modified ganglioside
20	573	86.7	128	14	AA28670	Rat immunoglobulin
21	566	85.6	128	20	AA28670	pK641 LA2 immunog
22	559	84.6	128	15	AA28670	K641 H chain vari
23	556	84.1	127	18	AA28670	Light chain variab
24	537	81.2	634	24	AA28670	CD19:zeta chimeric
25	534	80.8	107	24	AA28670	Ganglioside-associ
26	534	80.8	107	24	AA28670	Ganglioside-associ
27	534	80.8	108	22	AA28670	Murine consensus 1
28	533	80.6	128	22	AA28670	Ganglioside GD3 sp
29	526	79.6	107	19	AA28670	anti-CD22 monoclon
30	526	79.6	128	22	AA28670	Ganglioside GD3 sp
31	526	79.6	233	22	AA28670	Chimeric 4H6 anti-
32	525	79.4	128	22	AA28670	Ganglioside GD3 sp
33	525	79.4	895	23	AA28670	Diphtheria toxin/U
34	525	79.4	895	23	AA28670	Diphtheria toxin/U
35	525	79.4	895	23	AA28670	Diphtheria toxin/U
36	525	79.4	896	23	AA28670	Diphtheria toxin/U
37	525	79.4	896	23	AA28670	Diphtheria toxin/U
38	525	79.4	896	23	AA28670	Diphtheria toxin/U
39	525	79.4	899	23	AA28670	Diphtheria toxin/U
40	524	79.3	107	14	AA28670	Murine anti-CD3 MA
41	524	79.3	601	21	AA28670	An immunotoxin com
42	524	79.3	601	24	AA28670	Recombinant immuno
43	524	79.3	637	23	AA28670	Diphtheria toxin/U
44	524	79.3	638	23	AA28670	Diphtheria toxin/U
45	524	79.3	642	23	AA28670	Diphtheria toxin/U

ALIGNMENTS

RESULT 1
AA28670.
ID AA28670 standard; Protein; 127 AA.

AC	AA28670;				
XX					
DT	25-MAR-2003 (updated)				
DT	30-MAR-1993 (first entry)				
XX					
DE	pPM-k3 protein product.				
XX					
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;				
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;				
KW	plasmid; pPM-k3; pPM-h1.				
XX					
OS	Synthetic.				
XX					
PH	Key	Location/Qualifiers			
FT	Peptide	1..20			
FT		/note= "Signal peptide"			
FT	Protein	21..127			
FT		/note= "Mature peptide"			
XX					
PN	WO9219759-A1.				
XX					
PD	12-NOV-1992.				
XX					
PF	24-APR-1992;	92WO-JP00544.			
XX					
PR	25-APR-1991;	91JP-0095476.			
XX	19-FEB-1992;	92JP-0032084.			
XX					

```

PA (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX WPI; 1992-398882/48.
DR N-PSDB; AAQ30755.
XX
XX Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
XX
XX Disclosure; Page 121-122; 207pp; Japanese.
XX
XX The sequences given in AAR28670-71 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 127 AA;
SQ
Query Match 100.0%; Score 681; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3e-43;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
DB 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
QY 121 GTKLEIN 127
DB 121 GTKLEIN 127
RESULT 2
AAR84553
ID AAR84553 standard; Protein; 131 AA.
XX
XX AAR84553;
XX
XX 02-FEB-1996 (first entry)
XX
XX MAB SCH94.03 light chain.
XX
XX Monoclonal antibody; MAB; SCH94.03; hybridoma; central nervous system;
KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /label= Leader_peptide
FT Region 44..54
FT /label= CDR1
FT Region 70..76
FT /label= CDR2
FT Region 109..117
FT /label= CDR3
FT Region 116..128
FT /label= Joining_region
FT Region 129..131
FT /label= C-kappa_region
XX
XX WO9530004-A1.
XX
XX 09-NOV-1995.
XX
XX

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PF 27-APR-1995; 95WO-US05262.
XX
XX 29-APR-1994; 94US-0236520.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Miller DJ, Rodriguez M;
XX
XX WPI; 1995-393077/50.
DR N-PSDB; AAR05311.
XX
XX Monoclonal antibodies which stimulate central nervous system
PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT treating multiple sclerosis, and viral or post-neural diseases of
PT the CNS.
XX
XX Disclosure; Page 36-37; 63pp; English.
XX
XX Hybridoma ATCC CRL 11627 was obt'd. from a SJL/J mouse injected with
CC spinal cord homogenate from a mammal uninfected with any
CC demyelinating disease. The hybridoma produced a monoclonal antibody
CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC light chain amino acid sequence is given in AAR84553.
XX
XX Sequence 131 AA;
SQ
Query Match 96.5%; Score 638; DB 16; Length 131;
Best Local Similarity 96.0%; Pred. No. 7.8e-42;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
DB 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120
QY 121 GTKLEI 126
DB 121 GTKLEI 126
RESULT 3
AAR32121
ID AAR32121 standard; Protein; 127 AA.
XX
XX AAR32121;
XX
XX 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 02-JUN-1993 (first entry)
XX
XX Anti-CD4 antibody MT 15.1 light chain variable region.
XX
XX immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAB;
KW interleukin-2 receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /label= signal
FT Region 21..115
FT /label= Variable
FT Region 116..127
FT /label= J2
XX
XX DE4143214-A1.
XX
XX 28-JAN-1993.
XX
XX

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PF 30-DEC-1991; 91DE-4143214.
XX
XX 25-JUL-1991; 91DE-4124759.
PR 30-DEC-1991; 91DE-4143214.
XX
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
XX Kaluza B, Riethmueller G, Scheuer W, Weidle U;
XX
XX WPI; 1993-037582/05.
DR N-PSDB; AAQ36607.
XX
XX Synergistic antibody compen. for use as immunosuppressant -
FT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
FT alpha- or anti-IL2R beta antibodies
XX
XX Claim 5; Page 9; 18pp; German.
XX
XX This sequence is the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. MAB MT 15.1 is deposited as clone 15-1/P3/14 (ECACC
CC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See also AAQ36608-Q36616.
CC (Updated on 10-MAR-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 127 AA;
XX
XX Query Match 94.9%; Score 627; DB 14; Length 127;
XX Best Local Similarity 93.7%; Pred. No. 5.3e-41;
XX Matches 118; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Db 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDINNLSWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPTFTGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPTFTGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
XX
RESULT 4
AAW11815
ID AAW11815 standard; Protein; 127 AA.
XX
XX AC AAW11815;
XX
XX 20-OCT-1997 (first entry)
XX
XX Mouse anti-human Fas ligand antibody F919 light chain.
XX
XX Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
XX induction; assay; enzyme linked immunosorbant assay; diagnosis;
XX disease; hepatitis B; hepatitis C; human immunodeficiency virus;
XX graft versus host disease; ulcerative colitis; sequelae;
XX myocardial infarction; mouse; murine; monoclonal; treatment;
XX complementarity determining region; CDR.
XX
XX Mus spp.
XX
XX Key Location/Qualifiers
XX Region. 44..54
XX /label= CDR_1
XX Region 70..76
XX

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FT FT Region /label= CDR_2
FT FT 109..117
XX XX /label= CDR_3
XX WO9702290-A1.
XX 23-JAN-1997.
XX
XX 01-JUL-1996; 96WO-JP01820.
XX
XX 17-MAY-1996; 96US-0649100.
PR 30-JUN-1995; 95JP-0188480.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
XX
XX WPI; 1997-108917/10.
DR N-PSDB; AAT59500.
XX
XX Antibody reactive with Fas ligand capable of inducing apoptosis -
XX used for diagnostic assay of Fas ligand in body fluids and for
XX treatment of diseases in which Fas ligand/Fas antigen is involved
XX
XX Claim 5; Fig 10; 164pp; Japanese.
XX
XX The present sequence is the light chain of the mouse
XX anti-apoptosis inducing human Fas ligand, monoclonal antibody,
XX F919. The antibody can be used in a Fas ligand assay, e.g. an
XX enzyme linked immunosorbant assay, to diagnose diseases in which
XX the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
XX B/C, human immunodeficiency virus, graft/host disorders,
XX ulcerative colitis or sequelae of myocardial infarction. The
XX antibody may also be used to treat such diseases.
XX
XX SQ Sequence 127 AA;
XX
XX Query Match 93.9%; Score 621; DB 18; Length 127;
XX Best Local Similarity 93.7%; Pred. No. 1.5e-40;
XX Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Db 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPTFTGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDVATYFCQCGNTLPTFTGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
XX
RESULT 5
AAW60033
ID AAW60033 standard; Protein; 127 AA.
XX
XX AC AAW60033;
XX
XX 11-SEP-1998 (first entry)
XX
XX Mouse antibody F919-9-18 light chain sequence.
XX
XX Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
XX heart failure; kidney failure; graft-versus-host disease; antibody;
XX myocardial infarction; ischemic restenosis; endotoxic shock.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Region 44..54
XX

```


XX Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
 KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
 KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
 XX Mus sp.
 XX US5576184-A.
 XX 19-NOV-1996.
 XX 27-DEC-1994; 94US-0364001.
 XX 06-MAY-1991; 91US-0659401.
 XX 06-SEP-1988; 88US-0240624.
 XX 08-SEP-1988; 88US-0241744.
 XX 13-SEP-1988; 88US-0243739.
 XX 04-OCT-1988; 88US-0253002.
 XX 19-JUN-1989; 89US-0367641.
 XX 21-JUL-1989; 89US-0382768.
 XX 27-DEC-1994; 94US-0364001.
 XX (XOMA) XOMA CORP.
 XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
 XX WPI; 1997-011249/01.
 XX N-PSDB; AAT43440.
 XX Chimeric mouse-human antibodies - recognise a human tumour antigen,
 PT used for the treatment and diagnosis of human cancers
 XX Example 3; Fig 29; 102pp; English.
 XX The light chain variable region (AAW06215) of mouse monoclonal
 CC antibody ME4 is the product of a cDNA clone (AAT43440) isolated
 CC from a ME4 hybridoma cDNA library. MAB ME4 (IgG1) binds to an
 CC antigen that is expressed on the surface of human lung, breast,
 CC colon and ovary carcinomas and melanomas, but not on most normal
 CC adult tissues. The light chain and heavy chain variable regions
 CC (see also AAW06216) of ME4 can be linked to human constant regions
 CC and expressed in transformed host cells. Novel mouse-human
 CC chimeric antibodies (see also AAW06209-14 and AAW06217-18) can be
 CC produced that have specificity to human tumour antigens for use in
 CC the treatment and diagnosis of human cancer.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 128 AA;
 Query Match 93.9%; Score 621; DB 18; Length 128;
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
 Db 1 MMSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDIITLYLNWYQOKP 60
 Qy 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
 Db 61 DGTVKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPRTFGG 120
 Qy 121 GTKLEI 126
 Db 121 GTKLEI 126
 RESULT 8
 ID AAW85062 standard; Protein; 128 AA.
 XX AAW85062;
 AC AAW85062;
 XX 20-MAR-2003 (updated)

DT 16-APR-1999 (first entry)
 XX Mouse ME4 light chain variable region.
 DE Light chain variable region; murine antibody ME4; antibody ING-1;
 KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
 KW treatment; human cancer.
 XX Mus sp.
 XX US5843685-A.
 XX 01-DEC-1998.
 XX 06-JUN-1995; 95US-0466034.
 XX 06-SEP-1989; 89WO-US03852.
 XX 06-MAY-1991; 91US-0659401.
 XX 27-DEC-1994; 94US-0364001.
 XX 06-SEP-1988; 88US-0240624.
 XX 08-SEP-1988; 88US-0241744.
 XX 13-SEP-1988; 88US-0243739.
 XX 04-OCT-1988; 88US-0253002.
 XX 19-JUN-1989; 89US-0367641.
 XX 21-JUL-1989; 89US-0382768.
 XX (XOMA) XOMA CORP.
 XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
 XX WPI; 1999-044574/04.
 XX N-PSDB; AAV71158.
 XX Chimeric antibody specific for human tumour antigen - useful as
 PT immunoassay, imaging or antitumour agent
 XX Example 3; Fig 29; 92pp; English.
 XX The present sequence represents the light chain variable region of
 CC murine antibody ME4. The sequence was used to create chimeric
 CC mouse-human immunoglobulins which recognise the human tumour
 CC antigen bound by antibody ING-1 (produced by hybridoma cell line
 CC ATCC HB 9812). The chimeric antibodies also have an antigen-binding
 CC site that competitively inhibits the binding of antibody ING-1, and
 CC mediate complement-dependent cytotoxicity of target cells or
 CC antibody-dependent cellular cytotoxicity to target cells. The
 CC chimeric antibodies can be used for therapeutic purposes in the
 CC treatment of human cancer.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX SQ Sequence 128 AA;
 Query Match 93.9%; Score 621; DB 20; Length 128;
 Best Local Similarity 93.7%; Pred. No. 1.5e-40;
 Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
 Db 1 MMSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDIITLYLNWYQOKP 60
 Qy 61 DGTIKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
 Db 61 DGTVKLLIYVTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPRTFGG 120
 Qy 121 GTKLEI 126
 Db 121 GTKLEI 126
 RESULT 9
 ID ABUS8896 standard; Protein; 128 AA.
 XX ABUS8896
 XX

AC ABUS8896;
XX
DT 16-APR-2003 (first entry)
XX
DE Mouse antibody light chain variable region #4.
XX
DE MING; human tumour antigen; anti-human tumour antigen-antibody;
KW ING-1 antibody; cell line HB9812; immunoassay; imaging;
KW tumour diagnosis; tumour therapy; cytostatic;
KW light chain variable region.
XX
OS Mus sp.
XX
XX US6461824-B1.
PN
XX
XX 08-OCT-2002.
XX
XX 06-JUN-1995; 95US-0467142.
XX
PR 06-SEP-1989; 89US-0659401.
PR 06-SEP-1989; 89WO-US03852.
PR 27-DEC-1994; 94US-0364001.
PR 06-SEP-1988; 88US-0240624.
PR 08-SEP-1988; 88US-0241744.
PR 13-SEP-1988; 88US-0243739.
PR 04-OCT-1988; 88US-0253002.
PR 19-JUN-1989; 89US-0367641.
PR 21-JUL-1989; 89US-0382768.
XX
XX (XOMA) XOMA TECHNOLOGY LTD.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
PI
XX
XX WPI; 2003-196707/19.
DR N-PSDB; ABK79238.
DR
XX
XX Antibody for detecting antigen in animal or killing cells carrying
PT antigen comprises human constant region and variable region having
PT specificity for human tumor antigen bound by ING-1 antibody -
XX
XX Example 3; Fig 29; 101pp; English.
XX
XX The invention describes an antibody comprising a human constant region
CC and a variable region having specificity for the human tumour antigen
CC bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC HB9812 as deposited with ATCC, and the antibody has the same affinity as
CC the ING-1 for the human tumour antigen. The antibody is useful in an
CC immunoassay method for detecting an antigen in a sample by contacting a
CC label-detectable antigen in the sample with the antibody, detecting the
CC label and relating the detected label to the presence of the antigen; for
CC use in an imaging method for revealing the presence of a label-detectable
CC antigen in an animal by contacting the antibody with a part of the animal
CC suspected of containing the antigen, detecting the label and relating the
CC detected label to the presence of the antigen; and for killing cells
CC carrying an antigen by contacting the cells with the antibody and
CC allowing the killing to occur. The antibodies are useful in tumour
CC diagnosis and therapy. The chimeric antibodies bind to the surface of
CC human tumour cells but do not bind detectably to normal cells, e.g.,
CC fibroblasts, endothelial cells or epithelial cells in the major organs.
CC The high biological activity of the chimeric antibodies against human
CC tumour cell lines combined with minimal reactivity with normal tissues
CC imply that these antibodies may mediate selective destruction of
CC malignant tissue. The presence of human rather than murine antigenic
CC determinants on the chimeric antibodies increases their resistance to
CC rapid clearance from the body relative to the original murine mAbs. This
CC resistance to clearance enhances the potential utility of these chimeric
CC antibodies, as well as their derivatives, in tumour diagnosis and
CC therapy. This is the amino acid sequence of a mouse antibody light chain
CC variable region used in the creation of an anti-human tumour
CC antigen-antibody.
XX
SQ Sequence 128 AA;

Query Match 93.9%; Score 621; DB 24; Length 128;
Best Local Similarity 93.7%; Pred. No. 1.5e-40;
Matches 118; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLSDRVITISCRASQDITTLNMYQOKP 60
DB 1 MVSSAQFLGLLLCFQGTTRCDIQMTQTSSLSASLSDRVITISCRASQDITTLNMYQOKP 60
QY 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQGNLTPLYTFGG 120
DB 61 DGTIKLIYYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQGNLTPLYTFGG 120
QY 121 GTKLEI 126
DB 121 GTKLEI 126
RESULT 10
AAR39265
ID AAR39265 standard; Protein; 127 AA.
XX
AC AAR39265;
XX
DT 25-MAR-2003 (updated)
DT 29-NOV-1993 (first entry)
XX
DE Mouse C4G1 Ig light-chain.
XX
KW Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= signal_peptide
FT Protein 22..127
FT /label= light_chain
FT Region 44..54
FT /label= complementarity_determining_region_1
FT Region 70..76
FT /label= CDR_2
FT Region 109..117
FT /label= CDR_3
XX
XX WO9313133-A1.
XX
XX 08-JUL-1993.
XX
XX 15-DEC-1992; 92WO-JP01630.
XX
XX 20-DEC-1991; 91US-0812111.
XX
XX 09-JUN-1992; 92US-0895952.
XX
XX 11-SEP-1992; 92US-0944159.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX Co MS, Tso JY;
XX
XX WPI; 1993-227275/28.
XX
XX N-PSDB; AAQ45662.
XX
XX Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA
XX protein - for treating disorders related to vascular thrombosis
XX
XX Disclosure; Fig 2A; 54pp; Japanese.
XX
XX This is the sequence of the mouse C4G1 immunoglobulin light
XX chain. See AAR39266 for the heavy chain sequence. The antibody is
XX specific for the GPIIb/III protein and inhibits platelet
XX agglutination. The Ig is thus useful in the treatment of
XX thrombosis.

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CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 127 AA;

Query Match 93.6%; Score 619; DB 14; Length 127;
Best Local Similarity 92.9%; Pred. No. 2.2e-40;
Matches 117; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGLLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDINNLYLNWYQOKP 60

Qy 61 DGTIKLIYYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120
Db 61 DGIVKLLIYYTSLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPWTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 11
RAW49809
ID AA49809 standard; Protein; 127 AA.
AC AAW49809;
XX
DT 25-MAR-2003 (updated)
DT 24-SEP-1998 (first entry)
XX
DE Variable region of mouse antibody C4G1 light chain.
XX
KW Mouse; antibody C4G1; light chain; humanised; immunoglobulin; Ig;
KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW cancer; acute myocardial infarction; unstable angina; stroke;
KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW extracorporeal cardiopulmonary circulation.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein 21..127
FT Domain /note= "mature protein"
FT Domain 44..54
FT Domain /note= "complementarity determining region"
FT Domain 70..76
FT Domain /note= "complementarity determining region"
FT Domain 109..117
FT Domain /note= "complementarity determining region"
XX
PN US5777085-A.
XX
XX 07-JUL-1998.
XX
XX 17-MAY-1995; 95US-0458516.
XX
XX 03-MAY-1993; 91US-0059159.
XX 20-DEC-1991; 91US-0812111.
XX 09-JUN-1992; 92US-0895952.
XX 11-SEP-1992; 92US-0944159.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
PA (YAWA) YAMANOUCHI PHARM CO LTD.
XX
XX Co MS, Tso JY;
XX
XX WPI; 1998-398136/34.
XX N-PSDB; AAV36741.
XX
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
XX mouse C4G1 antibody, used for inhibiting platelet aggregation for
XX treating cardiovascular and thromboembolic disorders.
XX

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XX Disclosure; Fig 2A; 35pp; English.
XX
CC This is the amino acid sequence of the mouse antibody C4G1 light
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 127 AA;

Query Match 93.6%; Score 619; DB 19; Length 127;
Best Local Similarity 92.9%; Pred. No. 2.2e-40;
Matches 117; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGLLLLCFQGTQRCDIQMTQTSSLSASLGDRVTISCRASQDINNLYLNWYQOKP 60

Qy 61 DGTIKLIYYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPYTFGG 120
Db 61 DGIVKLLIYYTSLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPWTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 12
AAR99003
ID AAR99003 standard; Protein; 127 AA.
AC AAR99003;
XX
XX 10-JAN-1997 (first entry)
XX
XX Mab VIL1756 light chain (specific for human alphav integrins).
XX
XX Monoclonal antibody; Mab; integrin; cell-matrix interaction;
XX tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
XX imaging; detection; radiolabel.
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 21..43
FT Binding-site /label= Framework region 1
FT Region 44..54
FT Binding-site /label= CDR1
FT Region 55..69
FT Binding-site /label= Framework region 2
FT Region 70..76
FT Binding-site /label= CDR2
FT Region 77..108
FT Binding-site /label= Framework region 3
FT Region 109..117
FT Binding-site /label= CDR3
FT Region 118..127
FT Binding-site /label= Framework region 4
XX
XX EP719859-A1.
XX
XX 03-JUL-1996.
XX
XX 06-DEC-1995; 95EP-0119233.
XX

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XX 20-DEC-1994; 94EP-0120165.
PR (MERE ) MERCK PATENT GMBH.
PA
XX Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;
PI Rosell E;
PI
XX WPI: 1996-302345/31.
DR N-PSDB; AAT35050.
DR
XX New human integrin V chain-specific monoclonal antibody - and
PT related DNA and hybridomas, for treatment and diagnostic imaging of
PT tumours, esp melanoma.
PT
XX Claim 8; Figure 17a; 54pp; English.
PS
XX A monoclonal antibody which reacts only with the alphav chain of
CC human alphav integrins; which blocks attachment of alphav integrin
CC bearing cells to integrin substrate; which reverses established cell
CC matrix interactions caused by alphav integrin; which blocks tumour
CC development and which has no cytotoxic activity; may be used to
CC treat tumours, especially melanoma (but also glioma, carcinoma)
CC optionally coupled to a cytokine such as interleukin-2. The
CC monoclonal antibody may also be used for diagnostic imaging of
CC tumours and assessment of tumour growth when conjugated to a
CC radiolabel or a radio opaque-agent.
XX
SQ Sequence 127 AA;
Query Match 91.7%; Score 606; DB 17; Length 127;
Best Local Similarity 90.5%; Pred. No. 2.2e-39;
Matches 114; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCOQGNTPYTFGG 120
DB 61 DGTVKLLIFYTSKLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCOQGNTPYTFGG 120
QY 121 GTKLEI 126
DB 121 GTKVEM 126
RESULT 13
AAR29010
ID AAR29010 standard; Protein; 127 AA.
XX
AC AAR29010;
XX
DT 25-MAR-2003 (updated)
DT 30-MAR-1993 (first entry)
XX
DE p146-k3 protein product.
XX
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
KW plasmid; p146-k3; p146-h1.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..127
FT /note= "Mature peptide"
XX
PN WO9219759-A1.
XX
XX 12-NOV-1992.

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XX 24-APR-1992; 92WO-JP00544.
PF
XX 25-APR-1991; 91JP-0095476.
PR 19-FEB-1992; 92JP-0032084.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
PI
XX WPI; 1992-398882/48.
DR N-PSDB; AAQ30759.
DR
XX Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PT
XX Disclosure; Page 127-128; 207pp; Japanese.
PS
XX The sequences given in AAR29010-11 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody which
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 127 AA;
Query Match 90.6%; Score 599; DB 13; Length 127;
Best Local Similarity 90.5%; Pred. No. 7.5e-39;
Matches 114; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
DB 1 MVSTPQFLGLLVICFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCOQGNTPYTFGG 120
DB 61 DGTVKLLIYTSRLHSGVPSRFGSGGTDYSLTINNLEQEDIATYFCOQGNTPYTFGG 120
QY 121 GTKLEI 126
DB 121 GTKLEI 126
RESULT 14
AAR12237
ID AAR12237 standard; Protein; 126 AA.
XX
AC AAR12237;
XX
DT 25-MAR-2003 (updated)
DT 19-AUG-1991 (first entry)
XX
DE Mouse MAb 1C11 L chain, V region.
XX
KW HIV-1; chimera.
XX
OS Mus sp.
XX
PN WO9107494-A.
XX
XX 30-MAY-1991.
XX
PF 13-NOV-1990; 90WO-US06627.
PR 13-NOV-1989; 89US-0433703.
XX
XX (XOMA ) XOMA CORP.
PA (GREC ) GREEN CROSS CORP.
PA (ZOMA-) ZOMA CORP.
XX

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PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX WPI; 1991-178106/24.
XX N-PSDB; AAQ12017.
XX New chimeric mouse human antibodies - used in treatment, diagnosis
PT and prophylaxis of HIV infections.
XX
XX Disclosure; Fig 13; 108pp; English.
XX
XX The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 126 AA;
Query Match 89.3%; Score 590; DB 12; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.7e-38;
Matches 113; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Db 1 MMSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQGISNYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126
RESULT 15
AAR12359
ID AAR12359 standard; Protein; 127 AA.
XX
AC AAR12359;
XX
XX 25-MAR-2003 (updated)
DT 15-AUG-1991 (first entry)
XX
DE Light (kappa) chain variable region of murine 1C11 immunoglobulin.
XX
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
XX Mus musculus.
XX
XX W09107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1990; 90WO-US06615.
XX
XX 13-NOV-1989; 89US-0433730.
XX
XX (XOMA ) XOMA CORP.
XX (GREC ) GREEN CROSS CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX
XX WPI; 1991-178105/24.
XX N-PSDB; AAQ12061.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and
PT remove HIV-1 antigen from sample
XX
XX Disclosure; fig 13; 107pp; English.
XX

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CC This is the light (kappa)- chain variable (V) region of a mouse
CC monoclonal antibody (MAB), 1C11, and is specific for an HIV-1
CC viral antigen. It is used in the construction of a chimeric
CC MAB comprising heavy and light chains having murine V regions
CC and human C regions. The chimeric MABs are more effective than
CC murine MAB 1C11 since they have an increased compatibility in
CC humans. The heavy and light chain V-regions are joined by
CC manipulating their respective joining (J) regions, to generate
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV.
CC See also AAQ12056-60 and AAQ12062-63.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 127 AA;

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```

Query Match 89.3%; Score 590; DB 12; Length 127;
Best Local Similarity 89.7%; Pred. No. 3.7e-38;
Matches 113; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP 60
Db 1 MMSSAQFLGILLLCFQGTTRCDIQMTQTSSLSASLGDRVTISCRASQGISNYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGSGTDYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

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Search completed: October 22, 2003, 22:16:35
Job time : 59.2462 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:50 ; Search time 24.053 Seconds
(without alignments)
507.771 Million cell updates/sec

Title: US-09-114-285A-29
Perfect score: 661
Sequence: 1 MVSSAQFLGLLLLCFQGTTC.....CQCGNTLPYTFGGTKLEIN 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632	95.6	126	2 A34904	Ig kappa chain pre
2	627	94.9	127	2 PH1224	Ig kappa chain pre
3	625	94.6	128	2 A26406	Ig kappa chain V r
4	607	91.8	122	2 A29380	Ig kappa chain pre
5	584	88.4	115	2 A53276	Ig kappa chain V r
6	579	87.6	115	2 JL0080	Ig kappa chain pre
7	543	82.1	108	2 S69903	Ig kappa chain (cl
8	538	81.4	108	2 S69900	Ig kappa chain (cl
9	530	80.2	108	1 KWSAR	Ig kappa chain V r
10	529	80.0	107	2 B28044	Ig kappa chain V r
11	529	80.0	107	2 A28044	Ig kappa chain V r
12	527	79.7	108	2 S19970	Ig kappa chain V r
13	527	79.7	108	2 S69902	Ig kappa chain (cl
14	524	79.3	109	2 PH0888	Ig kappa chain V r
15	523.5	79.2	108	2 S38862	Ig kappa chain V r
16	520.5	78.7	107	2 S69901	Ig kappa chain (cl
17	516.5	78.1	107	2 S69906	Ig kappa chain (cl
18	516	78.1	107	2 S32188	Ig kappa chain V r
19	513	77.6	108	2 B26405	Ig kappa chain V r
20	512	77.5	108	2 C26405	Ig kappa chain V r
21	512	77.5	108	2 PH0282	Ig kappa chain V r
22	511	77.3	108	2 S11124	Ig kappa chain V r
23	507	76.7	107	2 B48677	Ig kappa chain V-J
24	505	76.4	107	2 B49026	Ig kappa chain V r
25	504	76.2	105	2 PH0087	Ig kappa chain V r
26	485	73.4	108	2 B30551	Ig kappa chain V r
27	485	73.4	111	2 A38740	Ig kappa chain V r
28	480	72.6	107	2 A48677	Ig kappa chain V-J
29	480	72.6	107	2 B48677	Ig kappa chain V-J

ALIGNMENTS

RESULT 1

A34904

Ig kappa chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000

C;Accession: A34904

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reacting antibodies

A;Reference number: A34903; PMID:90094387; PMID:2104617

A;Accession: A34904

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-126 <BED>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-109/Domain: immunoglobulin homology <IMV>

Query Match 95.6%; Score 632; DB 2; Length 126;

Best Local Similarity 93.7%; Pred. No. 2.3e-48;

Matches 118; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSSAQFLGLLLCFQGTTCDIQMTTSSLSASLGDRVTISCRASQDISSYLNWYQKPD 61

Db 1 MSSAQFLGLLLCFQGTTCDIQMTTSSLSASLGDRVTISCRASQDINNVLNMYQKPD 60

Qy 62 GTKLLIYYTSRLHSGVPSRFGSGGSDTSLTINNLEQEDATYFCQGNLTLPYTFGGG 121

Db 61 GTVKLLIYYTSKLHSGVPSRFGSGGSDTSLTISNLEQEDATYFCQGNLTLPYTFGGG 120

Qy 122 TKLEIN 127

Db 121 TKLEIN 126

RESULT 2

PH1224

Ig kappa chain precursor V region (M-T151) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000

C;Accession: PH1224

R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz

Gene 121, 271-278, 1992

A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on

A;Reference number: PH1224; PMID:93077041; PMID:1446824

A;Accession: PH1224

A;Molecule type: mRNA

A;Residues: 1-127 <WEI>

A;Cross-references: GB:S50261; NID:g260761; PIDN:AAB24318.1; PID:g260762

A;Note: this mouse sequence was hybridized and fused with a human constant region gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY3>
A;Cross-references: EMBL:X55049; NID:g511039; PIDN:CAA38889.1; PID:g511040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMW>

Query Match 81.4%; Score 538; DB 2; Length 108;
Best Local Similarity 96.2%; Pred. No. 3.2e-40;
Matches 102; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 21 DIQMTTSSLSASLGDRVTISCRASQDISSNLYNQKPDGTIKLLIYYTSLRLHSGVPS 80
Db 1 DIQMTTSSLSASLGDRVTISCRASQDISSNLYNQKPDGTIKLLIYYTSLRLHSGVPS 60
Qy 81 RFGSGSGTDYSLTINLNQEDVIATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTDYSLTINLNQEDVIATYFCQGNLTLPYTFGGGTKLEI 106

RESULT 9
KWMSAR
Ig kappa chain V regions (anti-arsonate hybridoma proteins) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 21-Jan-2000
C;Accession: A01927
R;Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A;Title: Complete amino acid sequence of light chain variable regions derived from five
A;Reference number: A01927; MUID:82150934; PMID:6801658
A;Accession: A01927
A;Molecule type: protein
A;Residues: 1-108 <SIE>
A;Experimental source: strain A/J
A;Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and Arg, 84-Ser, and 93-Ala
C;Comment: The sequence shown is HP R16.7.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMW>
F;23-88/Disulfide bonds: #status predicted

Query Match 80.2%; Score 530; DB 1; Length 108;
Best Local Similarity 95.3%; Pred. No. 1.6e-39;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 21 DIQMTTSSLSASLGDRVTISCRASQDISSNLYNQKPDGTIKLLIYYTSLRLHSGVPS 80
Db 1 DIQMTTSSLSASLGDRVTISCRASQDISSNLYNQKPDGTIKLLIYYTSLRLHSGVPS 60
Qy 81 RFGSGSGTDYSLTINLNQEDVIATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTDYSLTINLNQEDVIATYFCQGNLTLPYTFGGGTKLEI 106

RESULT 10
B28044
Ig kappa chain V region (GP1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
C;Accession: B28044
R;Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
A;Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
A;Reference number: A94179; MUID:87317629; PMID:3114744
A;Accession: B28044
A;Molecule type: mRNA
A;Residues: 1-107 <MEE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMW>

Query Match 80.0%; Score 529; DB 2; Length 107;
 Best Local Similarity 95.3%; Pred. No. 1.9e-39;
 Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVAISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPRTFGGTKLEI 106
 |||||

RESULT 11
 A28044
 Ig kappa chain V region (22B5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
 C:Accession: A28044
 R:Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
 A:Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
 A:Reference number: A94179; MUID:87317629; PMID:3114744
 A:Accession: A28044
 A:Molecule type: mRNA
 A:Residues: 1-107 <MEE>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 529; DB 2; Length 107;
 Best Local Similarity 95.3%; Pred. No. 1.9e-39;
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGKTLPRTFGGGTKLEI 106
 |||||

RESULT 12
 S19970
 Ig kappa chain V region (M-T151) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S19970
 R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992
 A:Description: Structural characterization of CD4 mAb.
 A:Reference number: S19963
 C:Keywords: heterotetramer; immunoglobulin
 A:Accession: S19970
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <WEI>
 A:Cross-references: EMBL:X65095; NID:G52286; PID:CAA46223.1; PID:G52287
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 527; DB 2; Length 108;
 Best Local Similarity 93.4%; Pred. No. 2.9e-39;
 Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDINNLSYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGKTLPRTFGGGTKLEI 106
 |||||

Query Match 79.7%; Score 527; DB 2; Length 108;
 Best Local Similarity 94.3%; Pred. No. 2.9e-39;
 Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPRTFGGTKLEI 106
 |||||

RESULT 14
 PH0888
 Ig kappa chain V region (anti-CD3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C:Accession: PH0888
 R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
 A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
 A:Reference number: PH0885; MUID:92113462; PMID:1346155
 A:Accession: PH0888
 A:Molecule type: mRNA
 A:Residues: 1-109 <SHA>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 524; DB 2; Length 109;
 Best Local Similarity 93.4%; Pred. No. 5.4e-39;
 Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDIRNLSYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 KFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPWTFGGTKLEI 106
 |||||

RESULT 15
 S38862
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S38862
 R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
 submitted to the EMBL Data Library, August 1993
 A:Description: Production and cloning of TMV-specific monoclonal antibodies.

Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 106

RESULT 13

S69902
 Ig kappa chain (clone KL2.28) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69902
 R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992
 A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin 4
 A:Reference number: S69900; MUID:92165291; PMID:1537587
 A:Accession: S69902
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <WYS>
 A:Cross-references: EMBL:X55043; NID:G511027; PID:CAA38883.1; PID:G511028
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 527; DB 2; Length 108;
 Best Local Similarity 94.3%; Pred. No. 2.9e-39;
 Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPRTFGGTKLEI 106
 |||||

RESULT 14

PH0888
 Ig kappa chain V region (anti-CD3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C:Accession: PH0888
 R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
 A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
 A:Reference number: PH0885; MUID:92113462; PMID:1346155
 A:Accession: PH0888
 A:Molecule type: mRNA
 A:Residues: 1-109 <SHA>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 524; DB 2; Length 109;
 Best Local Similarity 93.4%; Pred. No. 5.4e-39;
 Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYTSRLHSGVPS 80
 |||||
 Db 1 DIQMTQTTSSLSASLGDRVTISCRASQDIRNLSYQKPDGTIKLLIYTSRLHSGVPS 60
 |||||

Oy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
 |||||
 Db 61 KFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPWTFGGTKLEI 106
 |||||

RESULT 15

S38862
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S38862
 R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
 submitted to the EMBL Data Library, August 1993
 A:Description: Production and cloning of TMV-specific monoclonal antibodies.

A;Reference number: S37200
 A;Accession: S38862
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-108 <FIS>
 A;Cross-references: EMBL:X75854; NID:9429109; PID:9429110
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 523.5; DB 2; Length 108;
 Best Local Similarity 93.5%; Pred. No. 5.9e-39;
 Matches 100; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKPDGTIKLLIYYTSLRLHSGVPS 80
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 DVQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKPDGTIKLLIYYTSLRLHSGVPS 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Qy 81 RFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPWTFGGGTKLEI 126
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 RFGSGSGTDYSLTINNLEQEDATYFCQGNLTLPWTFGGGTKLEI 107
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: October 22, 2003, 22:18:05
 Job time : 25.053 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:10:20 ; Search time 12.9886 Seconds
(without alignments)
459.817 Million cell updates/sec

Title: US-09-114-285A-29
Perfect score: 661
Sequence: 1 MVSSAQFLGLLLCFOGTRC.....COQNTLPYTFGGTKLEIN 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	530	80.2	108	1 KV5K_MOUSE	P01644 mus musculu
2	528	79.9	108	1 KV5L_MOUSE	P01645 mus musculu
3	525	79.4	108	1 KV5N_MOUSE	P01647 mus musculu
4	516	78.1	108	1 KV5M_MOUSE	P01646 mus musculu
5	513	77.6	108	1 KV5O_MOUSE	P01648 mus musculu
6	499	75.5	108	1 KV5U_MOUSE	P04946 mus musculu
7	473	71.6	108	1 KV5J_MOUSE	P01643 mus musculu
8	451	68.2	130	1 KV5G_MOUSE	P01639 mus musculu
9	431	65.2	129	1 KV1W_HUMAN	P04431 homo sapien
10	416	62.9	128	1 KV5E_MOUSE	P01637 mus musculu
11	412	62.3	117	1 KV1I_HUMAN	P01601 homo sapien
12	406	61.4	108	1 KV5P_MOUSE	P01649 mus musculu
13	400	60.5	108	1 KV1O_HUMAN	P01607 homo sapien
14	400	60.5	129	1 KV1X_HUMAN	P04432 homo sapien
15	395	59.8	108	1 KV1Y_HUMAN	P03062 homo sapien
16	393	59.5	108	1 KV1P_HUMAN	P01608 homo sapien
17	387	58.5	108	1 KV1B_HUMAN	P01594 homo sapien
18	386	58.4	108	1 KV1A_HUMAN	P01593 homo sapien
19	384	58.1	117	1 KV1J_HUMAN	P01602 homo sapien
20	379	57.3	108	1 KV1E_HUMAN	P01597 homo sapien
21	377	57.0	108	1 KV1S_HUMAN	P01611 homo sapien
22	377	57.0	115	1 KV5F_MOUSE	P01638 mus musculu
23	376	56.9	108	1 KV1H_HUMAN	P01600 homo sapien
24	375	56.7	108	1 KV1N_HUMAN	P01605 homo sapien
25	374	56.6	108	1 KV1M_HUMAN	P01606 homo sapien
26	368	55.7	108	1 KV1L_HUMAN	P01604 homo sapien
27	367.5	55.6	107	1 KV1D_HUMAN	P01596 homo sapien
28	365	55.2	117	1 KV5H_MOUSE	P01641 mus musculu
29	364	55.1	108	1 KV1Q_HUMAN	P01609 homo sapien
30	364	55.1	108	1 KV1V_HUMAN	P04430 homo sapien
31	363	54.9	111	1 KV3L_MOUSE	P01664 mus musculu
32	362	54.8	108	1 KV1R_HUMAN	P01610 homo sapien
33	361	54.6	108	1 KV5S_MOUSE	P01652 mus musculu

34	361	54.6	111	1 KV3H_MOUSE	P01660 mus musculu
35	360	54.5	131	1 KV3I_MOUSE	P01661 mus musculu
36	358	54.2	108	1 KV5Q_MOUSE	P01650 mus musculu
37	358	54.2	136	1 KV5B_MOUSE	P01634 mus musculu
38	356	53.9	111	1 KV3M_MOUSE	P01665 mus musculu
39	358	53.7	111	1 KV3O_MOUSE	P01667 mus musculu
40	354.5	53.6	133	1 KV3E_HUMAN	P06313 homo sapien
41	354	53.6	108	1 KV1C_HUMAN	P01595 homo sapien
42	354	53.6	108	1 KV1K_HUMAN	P01603 homo sapien
43	354	53.6	108	1 KV5T_MOUSE	P01653 mus musculu
44	354	53.6	111	1 KV3R_MOUSE	P01670 mus musculu
45	354	53.6	134	1 KV4C_HUMAN	P06314 homo sapien

ALIGNMENTS

RESULT 1
KV5K_MOUSE STANDARD; PRT; 108 AA.
ID KV5K_MOUSE
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KMSAR.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; A554642C63EFF597 CRC64;
Query Match 80.2%; Score 530; DB 1; Length 108;
Best Local Similarity 95.3%; Pred. No. 2.6e-46;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy	21	DIQWTTTSSLSASLGRVITISCRASODISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS	80
Db	1	DIQWTTTSSLSASLGRVITISCRASODISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS	60
Qy	81	RFGSGSGTGYSLTINNLEQEDATYFCQGNLTPYTFGGTKLEI	126
Db	61	RFGSGSGTGYSLTINNLEQEDATYFCQGNLTPYTFGGTKLEI	106

RESULT 2

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KV5L MOUSE
ID KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
Query Match 79.9%; Score 528; DB 1; Length 108;
Best Local Similarity 95.3%; Pred. No. 4.2e-46;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 80
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106
RESULT 3
KV5M MOUSE
ID KV5M MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 123B6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
Query Match 79.4%; Score 525; DB 1; Length 108;
Best Local Similarity 94.3%; Pred. No. 8.3e-46;
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 80
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106
RESULT 4
KV5M MOUSE
ID KV5M MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 123B6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
Query Match 79.4%; Score 525; DB 1; Length 108;
Best Local Similarity 94.3%; Pred. No. 8.3e-46;
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 80
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106

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Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
Query Match 79.4%; Score 525; DB 1; Length 108;
Best Local Similarity 94.3%; Pred. No. 8.3e-46;
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 80
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106
RESULT 4
KV5M MOUSE
ID KV5M MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 123B6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT SEQUENCE
Query Match 79.4%; Score 525; DB 1; Length 108;
Best Local Similarity 94.3%; Pred. No. 8.3e-46;
Matches 100; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 80
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTLKLIYYTSRLHSGVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 126
DB 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTPTFGGGTKLEI 106

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Query Match 78.1%; Score 516; DB 1; Length 108;
Best Local Similarity 93.4%; Pred. No. 6.6e-45;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 106

RESULT 5
KV5U MOUSE
ID KV5U MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype." (1981).
CC Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;
Query Match 77.6%; Score 513; DB 1; Length 108;
Best Local Similarity 91.5%; Pred. No. 1.3e-44;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 106

RESULT 6
KV5U MOUSE
ID KV5U MOUSE STANDARD; PRT; 108 AA.
AC P04946;
```

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region NQS-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
RL Nature 304:320-324(1983).
CC -!- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC
CC EMBL; K00745; AAA38690.1; -.
CC HSSP; P01607; IREI.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;
Query Match 75.5%; Score 499; DB 1; Length 108;
Best Local Similarity 89.6%; Pred. No. 3.3e-43;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTTKLLIYVTSRLHSGVPS 60

Qy 81 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTDYSLTINLEQEDATYFCQGNLTLPYTFGGGTKLEI 106

RESULT 7
KV5J MOUSE
ID KV5J MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
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RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01926; KVM573.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT CHAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 FRAMEWORK-3.
FT DOMAIN 57 88 FRAMEWORK-4.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 71.6%; Score 473; DB 1; Length 108;
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQQKPDGTIKLLIYTSRLHSGVPS 80
DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQQKPDGTIKLLIYTSRLHSGVPS 60

QY 81 RFSGSGSGDYSLTNLEQEDIAITYFCQGNLTLPYTFGGGPKLEI 126
DB 61 RFSGSGSGDYSLTNLEQEDIAITYFCQGNLTLPYTFGGGPKLEI 106

RESULT 8
KV5G_MOUSE
ID KV5G_MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.B., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation.";
RL Nature 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Burstein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains.";
RL Science 155:465-467(1967).
CC -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE

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CC SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A93211; KVM5M4.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Bence-Jones protein.
FT SIGNAL 1 22
FT CHAIN 23 130 IG KAPPA CHAIN V-V REGION MOPC 41.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT VARIANT 1 12 MISSING (IN 25% OF THE MOLECULES).
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; 5EFE0FE71D5F1BEC CRC64;

Query Match 68.2%; Score 451; DB 1; Length 130;
Best Local Similarity 70.6%; Pred. No. 2.6e-38;
Matches 89; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQQK 60
DB 3 MRPAQIFGFLLLFQGTCDIQMTQTSSLSASLGDRVSLTCRASQDISYLNWYQQK 62

QY 61 DGTIKLIYTSRLHSGVPSRFSGSGSGDYSLTNLEQEDIAITYFCQGNLTLPYTFGG 120
DB 63 DGTIKLIYATSSLDGVPKRFSGSGSGDYSLTNLEQEDIAITYFCQGNLTLPYTFGG 122

QY 121 GTKLEI 126
DB 123 GTKLEI 128

RESULT 9
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUK.
DR HSSP; P01607; 1REI.

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DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding activity; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 65.2%; Score 431; DB 1; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.6e-36;
Matches 86; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 5 AQLGLLLLCFOGTRCDIOMTQTTSSLSASLGDVRTISCRASODISSVLNWOQKPGDTI 64
DB 7 AQLGLLLLRGARGCDIOMTQSPSSLSASVGDVRTITCRASQISNVLNWOQKPGAP 66
QY 65 KLIYYSRLHSGVPSRFGSGSGTDYSLTINNLEQEDYATFCQGNLTLPYTFGGTKL 124
DB 67 KLIYASLSGSGVTSRFGSGSGTDFTLTISSLPEDSATYTCQSYSLTIFGQGTSL 126
QY 125 EI 126
DB 127 EI 128

RESULT 10
KVSE_MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma.";
RL Nature 287:603-607(1980).
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CC
CC EMBL; V00772; CAA24150.1; -.
DR F01920; KVMST1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Query Match 62.9%; Score 416; DB 1; Length 128;
Best Local Similarity 63.5%; Pred. No. 8.1e-35;
Matches 80; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

QY 1 MVSSAQLGLLLCFOGTRCDIOMTQTTSSLSASLGDVRTISCRASODISSVLNWOQK 60
DB 1 MRPAPQFLGLLLWFFGKIDIKMTQSPSSMYASLGVRVTISCRASODINSYLTWFOQKP 60
QY 61 DGTIKLIYYSRLHSGVPSRFGSGSGTDYSLTINNLEQEDYATFCQGNLTLPYTFGG 120
DB 61 GKSPKTLVLRANLVDGVPSRFGSGSGDQFSLTISLSEYEDMGYYCLOYDFEPLTFGA 120
QY 121 GTKLEI 126
DB 121 GTKLEL 126

RESULT 11
KVII_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
CC
CC SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";
RL Cell 32:181-189(1983).
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CC
CC EMBL; K01322; AAA58930.1; -.
DR EMBL; K01324; AAA58932.1; -.

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FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 60.5%; Score 400; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 2.7e-33;
Matches 77; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 21 DIQMTTSSLSASIGDRVTTISCRASQDISSYLNWYQOKPGDTIKLLIYTSRLHSGVPS 80
Db 1 DIQMTQSPSSLSASIGDRVTTICQASQDIKYLWYQOTPGKAPKLLIYYSNLOQGVPS 60

Qy 81 RFGSGSGTGYSLTINNLEQEDATYFCQGNLTLPYTFGGGTKLEI 126
Db 61 RFGSGSGTGYTFTTSSISLPEDATYCYQQLSLPYTFGGGTKLQI 106

RESULT 14
KVIX HUMAN
ID KVIX HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00966; CA25478.1; ALT TERM.
DR PIR; A01884; KIHU01.
DR HSSP; P80362; 1WTL.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match 60.5%; Score 400; DB 1; Length 129;
Best Local Similarity 62.8%; Pred. No. 3.3e-33;
Matches 76; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 5 AQLGLLLLCFQGRCDIQMTTSSLSASIGDRVTTISCRASQDISSYLNWYQOKPGDTI 64
Db 7 AQLGLLLLLWRVRCDIQMTQSPSSLSASIGDRVTTICRAGHNITNPLSYQOKPGKAP 66

Qy 65 KLLIYTSRLHSGVPSRFGSGSGTGYSLTINNLEQEDATYFCQGNLTLPYTFGGGTKL 124
Db 67 TLLIYVSNLQGVPSRFGSGSGAEFTLTSSISLPEDATYCYQQLNYSFTFGGGTKV 126
Qy 125 E 125
Db 127 D 127

RESULT 15
KVIX HUMAN
ID KVIX HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-related fragment of the human kappa Bence Jones protein Wat."
RL J. Mol. Biol. 147:185-193(1991)
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
```

DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT CONFLICT 30 31
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 59.8%; Score 395; DB 1; Length 108;
Best Local Similarity 69.8%; Pred. No. 8.4e-33;
Matches 74; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLVNYYQKPDGTIKLLIYYTSLRLHSGVPS 80
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDITNVNWFQORPGQAPKVLIIYGASILETVPS 60
QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPVTFGGGTKLEI 126
DB 61 RFGSGSGTDFTFTISSLPEDIATYCCQYDTLPLTFGGGTKVDI 106

Search completed: October 22, 2003, 22:17:09
Job time : 13.9886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:13:15 ; Search time 58.2083 Seconds
(without alignments)
563.024 Million cell updates/sec

Title: US-09-114-285A-29
Perfect score: 661
Sequence: 1 MVSSAQLGLLLLCFQGTCTC.....COQGNLPTFTGGTGKLEIN 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			Description
	Score	Query Match %	Length DB ID	
1	613	92.7	234 11	Q91WF8 mus musculus
2	574	86.8	234 11	Q8R062 mus musculus
3	534	80.8	233 11	Q91WS9 mus musculus
4	441	66.7	127 11	Q925S9 mus musculus
5	430	65.1	107 11	Q9JL84 mus musculus
6	392.5	59.4	107 4	Q96SA9 mus musculus
7	390	59.0	108 4	Q9UL77 homo sapien
8	389	58.9	234 11	Q8VCP0 mus musculus
9	388	58.7	108 4	Q9UL70 homo sapien
10	370.5	56.1	107 4	Q9UL81 homo sapien
11	367	55.5	214 11	Q9RIA5 mus musculus
12	363	54.9	108 4	Q9UL79 mus musculus
13	361	54.9	111 11	Q920E9 mus musculus
14	351	53.1	108 11	Q8VJ70 mus musculus
15	348	52.6	116 4	Q96PF6 homo sapien
16	347	52.5	234 4	Q8NEK1 homo sapien

17	345.5	52.3	112	11	Q8K1F3	Q8klf3 mus musculus
18	345	52.2	101	11	Q9JL78	Q9jl78 mus musculus
19	344.5	52.1	114	11	Q8K1F1	Q8klf1 mus musculus
20	343	51.9	298	11	Q9QYF0	Q9qyf0 mus musculus
21	339	51.3	109	11	Q920E6	Q920e6 mus musculus
22	335.5	50.8	238	11	Q99M37	Q99m37 mus musculus
23	331.5	50.2	112	11	Q8K1F2	Q8klf2 mus musculus
24	331.5	50.2	134	11	Q8VDD0	Q8vdd0 mus musculus
25	329.5	49.8	238	11	Q8VC16	Q8vc16 mus musculus
26	329.5	49.8	239	4	Q8TCD0	Q8tcd0 homo sapien
27	329.5	49.8	239	11	Q8K0F8	Q8kof8 mus musculus
28	328	49.6	103	11	Q9JL80	Q9jl80 mus musculus
29	326	49.3	234	11	Q8R028	Q8r028 mus musculus
30	325.5	49.2	109	4	Q9UL78	Q9ul78 homo sapien
31	320.5	48.5	239	11	Q8VC55	Q8vc55 mus musculus
32	320	48.4	108	4	Q9UL83	Q9ul83 homo sapien
33	318.5	48.2	239	4	Q8NEK0	Q8nek0 homo sapien
34	316.5	47.9	106	5	Q9U410	Q9u410 schistosoma
35	316.5	47.9	241	11	Q921A6	Q921a6 mus musculus
36	313	47.4	99	11	Q9JL74	Q9jl74 mus musculus
37	312.5	47.3	109	4	Q9UL85	Q9ul85 homo sapien
38	311	47.0	97	11	Q9JL76	Q9jl76 mus musculus
39	308.5	46.7	104	11	Q9JL82	Q9jl82 mus musculus
40	307.5	46.5	235	11	Q91W12	Q91w12 mus musculus
41	307	46.4	107	11	Q9ER29	Q9er29 mus musculus
42	306.5	46.4	112	11	Q8K1F0	Q8klf0 mus musculus
43	300.5	45.5	109	4	Q9UL86	Q9ul86 homo sapien
44	285.5	43.2	148	11	Q8K122	Q8kl22 mus musculus
45	281	42.5	114	4	Q9UL80	Q9ul80 homo sapien

ALIGNMENTS

RESULT 1

Q91WF8	ID	Q91WF8	PRELIMINARY;	PRT;	234 AA.
AC	Q91WF8;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Hypothetical 25.9 kDa protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Colon;				
RA	Strausberg R.;				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC015292; AAH15292.1; .				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	InterPro; IPR001865; Ribosomal_S2.				
DR	Pfam; PF00047; IG; 2.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
DR	PROSITE; PS00962; RIBOSOMAL_S2_1; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 234 AA; B0D0B0E6EB7812D2 CRC64;				
Query Match 92.7%; Score 613; DB 11; Length 234;					
Best Local Similarity 92.1%; Pred. No. 3.5e-56;					
Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0;					
Qy	1	MVSSAQLGLLLLCFQGTCTC	QMTTSSLSASLSDRVITISCRASD	ISYLNWYQOKP	60
Db	1	MVSSAQLGLLLLCFQGTCTC	QMTTSSLSASLSDRVITISCRASD	ISYLNWYQOKP	60
Qy	61	DGTLKIYYTSRLHSGVPSRFGSGGT	YSYLTINNLEQEDATYFCQGNLPT	FTFGG	120
Db	61	DGTVKLLIYYTSRLYLGVPSPRFGSG	GTYSYLTISNLEQEDATYFCQGNL	PTFTFGS	120

```
QY 121 GTKLEI 126
Db 121 GTKLEV 126

RESULT 2
QBR062
ID QBR062 PRELIMINARY; PRT; 234 AA.
AC QBR062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 86.8%; Score 574; DB 11; Length 234;
Best Local Similarity 87.3%; Pred. No. 5.8e-54;
Matches 110; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQGISNLYNWOQKP 60

QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGS 120

QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 3
Q91WS9
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
```

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 80.8%; Score 534; DB 11; Length 233;
Best Local Similarity 87.1%; Pred. No. 1.2e-49;
Matches 101; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 11 LLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKPDGTIKLLIYY 70
Db 10 LLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQGISNLYNWOQPDGTIVKLLIYY 69

QY 71 TSLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGGGTKLEI 126
Db 70 TSLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGGGTKLEI 125
```

```
RESULT 4
Q92SS9
ID Q92SS9 PRELIMINARY; PRT; 127 AA.
AC Q92SS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF."
RL Hybridoma 18:193-202(1999).
DR EMBL; AF124721; AAK55120.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;

Query Match 66.7%; Score 441; DB 11; Length 127;
Best Local Similarity 69.8%; Pred. No. 6.4e-40;
Matches 88; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQOKP 60
Db 1 MRAPAQILGFLLLPFGTCDIQMTQSPSSLSASLGQRVSLTCRASODIGINHLWQOEP 60

QY 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDYSLTNINLEQEDIATYFCQOQNTLPTFTGG 120

QY 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 5
Q9JL84
ID Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84;
```

```
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206022; AAF69320.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACAL5SD CRC64;

Query Match 65.1%; Score 430; DB 11; Length 107;
Best Local Similarity 78.3%; Pred. No. 7.9e-39;
Matches 83; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGRVITISCRASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQSPSSLSASLGRVITITCRASQISSYLNWYQOKPKAPKLIYYAASSLSQSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOG-NTLPYTFGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOG-NTLPYTFGGGTKLEI 106

RESULT 6
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031 (1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 107
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SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 59.4%; Score 392.5; DB 4; Length 107;
Best Local Similarity 74.8%; Pred. No. 9.1e-35;
Matches 80; Conservative 11; Mismatches 13; Indels 3; Gaps 2;

Qy 21 DIQMTQTTSSLSASLGRVITISCRASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQSPSSLSASLGRVITITCRASQISSYLNWYQOKPKAPKLIYYAASSLSQSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOG-NTLPYTFGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOG-NTLPYTFGGGTKLEI 105

RESULT 7
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 59.0%; Score 390; DB 4; Length 108;
Best Local Similarity 71.7%; Pred. No. 1.7e-34;
Matches 76; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 21 DIQMTQTTSSLSASLGRVITISCRASQDISSYLNWYQOKPDGTIKLIYYTSRLHSGVPS 80
Db 1 DIQMTQSPSSLSASLGRVITITCRASQISSYLNWYQOKPKAPKLIYYAASSLSQSGVPS 60

Qy 81 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 126
Db 61 RFSGSGSGTDYSLTINNLEQEDVATYFCQOGNTLPYTFGGGTKLEI 106

RESULT 8
Q8VCP0 PRELIMINARY; PRT; 234 AA.
ID Q8VCP0
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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(1)
RN RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 58.9%; Score 389; DB 11; Length 234;
Best Local Similarity 61.2%; Pred.No. 6.1e-34;
Matches 74; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 6 QFLGLLLCFQGTTRCDIQMTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIK 65
DB 6 QVLGLLLCLTGARCDIQTPASLSASVGETVITCRASENIYSYLAWYQOKGKSPQ 65

QY 66 LLIIYTSRLHSGVPRFSGSGGTGYSLTINNLEQEDIATYFCQGNLTLPYTFGGTKLE 125
DB 66 LLIVNAKTLADGVPRFSGSRGTQFSKLKINSLOPEDFGSYCQHHSGIPFTFGSGTKLE 125

QY 126 I 126
DB 126 I 126

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 58.7%; Score 388; DB 4; Length 108;
Best Local Similarity 71.7%; Pred. No. 2.8e-34;
Matches 76; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 21 DIQMTQTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIKLLIYTSRLHSGVPS 80
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNLYAWYQKPGKVPKSLIYAASLTQSGVPS 60

QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGGTKLEI 126
DB 61 RFGSGSGTDFTLTISGLQAEEDFATYTCQSSYS-ALTFGPGTKYDI 105

RESULT 11
Q9RIAS PRELIMINARY; PRT; 214 AA.
ID Q9RIAS
AC Q9RIAS
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01679; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 RFGSGSGTDFTLTISGLQAEEDFATYTCQSSYSAPRTFGPGTKLEI 106

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81
AC Q9UL81
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 56.1%; Score 370.5; DB 4; Length 107;
Best Local Similarity 69.8%; Pred. No. 2.2e-32;
Matches 74; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

QY 21 DIQMTQTTSSLSASGLDRVTISCRASODISSYLNWYQOKPDGTIKLLIYTSRLHSGVPS 80
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNLYAWYQKPGKAPNLLIYAASLSQSGVPS 60

QY 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGGTKLEI 126
DB 61 RFGSGSGTDFTLTISGLQAEEDFATYTCQSSYS-ALTFGPGTKYDI 105

RESULT 11
Q9RIAS PRELIMINARY; PRT; 214 AA.
ID Q9RIAS
AC Q9RIAS
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01679; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.5%; Score 367; DB 11; Length 214;
Best Local Similarity 66.0%; Pred. No. 1.3e-31;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGRVITISCRASQDISSYLNWYQKQKPDGTTIKLIYYTSRLHSGVPS 80
Db 1 DIQLTQSPSSMYASLGRVITITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDCGVP 60

Qy 81 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 126
Db 61 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 106

RESULT 12
ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01697; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 54.9%; Score 363; DB 4; Length 108;
Best Local Similarity 69.8%; Pred. No. 1.4e-31;
Matches 74; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGRVITISCRASQDISSYLNWYQKQKPDGTTIKLIYYTSRLHSGVPS 80
Db 1 DIVMTQSPSSLSASLGRVITISCRMSQGISYLAWYQKPKAPPELLIYAATSLQSGVPS 60

Qy 81 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 126
Db 61 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 106

RESULT 13
Q920E9 PRELIMINARY; PRT; 111 AA.
ID Q920E9
AC Q920E9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.5%; Score 367; DB 11; Length 214;
Best Local Similarity 66.0%; Pred. No. 1.3e-31;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGRVITISCRASQDISSYLNWYQKQKPDGTTIKLIYYTSRLHSGVPS 80
Db 1 DIQLTQSPSSMYASLGRVITITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDCGVP 60

Qy 81 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 126
Db 61 RFGSGSGGTGYSLTNINLEQEDDIATYFCQGNNTLPYTFGGGTKEI 106

RESULT 14
ID Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Vki19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233 (1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 53.1%; Score 351; DB 11; Length 108;
Best Local Similarity 60.4%; Pred. No. 2.8e-30;
Matches 64; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
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QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYTSRLHSGVPS 80
Db 1 DIVMTQSTFMSTVSGDRVSVTCKASQNVGTWVWYQKPGQSPKALIYSASYPYSGVPH 60
QY 81 RFSGGSGTDYSLTINNLEQEDIATYFCQGNLTLPYFGGGTKLEI 126
Db 61 RFTGGSGGTDFTLTISNVQSEDLAEYFCQYNSYPYTFGGGKLEI 106

RESULT 15

Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden."
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 52.6%; Score 348; DB 4; Length 116;
Best Local Similarity 62.9%; Pred. No. 6.6e-30;
Matches 66; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYTSRLHSGVPS 80
Db 1 DIVMTQSTFMSTVSGDRVSVTCKASQNVGTWVWYQKPGQSPKALIYSASYPYSGVPH 60
QY 81 RFSGGSGTDYSLTINNLEQEDIATYFCQGNLTLPYFGGGTKLE 125
Db 61 RFTGGSGGTDFTLTISNVQSEDLAEYFCQYNSYPYTFGGGKLEI 106

Search completed: October 22, 2003, 22:20:15
Job time : 60.2083 secs


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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-29

Query Match      100.0%; Score 661; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120

Qy 121 GTKLEIN 127
Db 121 GTKLEIN 127

RESULT 2
US-08-436-717-29
; Sequence 29, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-29

Query Match      100.0%; Score 661; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120

Qy 121 GTKLEIN 127
Db 121 GTKLEIN 127

RESULT 3
US-08-236-520-2
; Sequence 2, Application US/08236520
; Patent No. 5591629
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,520
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 27,227
; REFERENCE/DOCKET NUMBER: MMV92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-520-2

Query Match      96.5%; Score 638; DB 1; Length 131;
Best Local Similarity 96.0%; Pred. No. 9.5e-59;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60
Db 1 MVSSAQFLGILLLCFQGTQCDIQMTQTSSLSASLGDRVTISCRASODISSYLNWYQKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFSGSGTDYSLTINNLEQEDIAITYFCQOQNTLPYTFGG 120
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Qy 121 GTKLEI 126
|
Db 121 GTKLEI 126

RESULT 4

PCT-US95-05262-2
; Sequence 2, Application PC/TUS9505262
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education Research
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/236,520
; FILING DATE: April 29, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 27,227
; REFERENCE/DOCKET NUMBER: MMV92-01 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-05262-2

Query Match 96.5%; Score 638; DB 5; Length 131;
Best Local Similarity 96.0%; Pred. No. 9,5e-59;
Matches 121; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
|
Db 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTDYSLTINNLEQDIATYFCQOGNTLPYTFGG 120
|
Db 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTDYSLTINNLEQDIATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
|
Db 121 GTKLEI 126

RESULT 5

US-08-649-100-17
; Sequence 17, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU

; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-17

Query Match 93.9%; Score 621; DB 3; Length 127;
Best Local Similarity 91.7%; Pred. No. 5.3e-57;
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
|
Db 1 MVSSAQFLGLLLCFQGTGRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
Qy 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTDYSLTINNLEQDIATYFCQOGNTLPYTFGG 120
|
Db 61 DGTIKLLIYVTSRLHSGVPSRFSGSGTDYSLTINNLEQDIATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
|
Db 121 GTKLEI 126

RESULT 6

US-08-458-516-5
; Sequence 5, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-137-117D-37

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Best Local Similarity 92.1%; Pred. No. 4.5e-56;
Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSAPFLGLLLCFQGTTRCDIQMTQTSSLSASLGRVITISCRASQDISYLNWYQKP 60
Db 1 MVSTPQFLGLLLCFQGTTRCDIQMTQTSSLSASLGRVITISCRASQDISYLNWYQKP 60
Qy 61 DGIKLLIYVTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIAITYFCQGNTPLPYTFGG 120
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Qy 121 GTKLEI 126
Db 121 GTKLEI 126

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RESULT 8
US-08-436-717-37
; Sequence 37, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544

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; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-37

Query Match 92.6%; Score 612; DB 2; Length 127;
Best Local Similarity 92.1%; Pred. No. 4.5e-56;
Matches 116; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTCTCDIQMTQTSSLSASLGRVITISCRASODISSYLNWYQOKP 60
Db 1 MVSTPQFLGLLLICFQGTCTCDIQMTQTSSLSASLGRVITISCRASODISSYLNWYQOKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 9
US-08-574-699A-2
; Sequence 2, Application US/08574699A
; Patent No. 5985278
; GENERAL INFORMATION:
; APPLICANT: MITJANS, Francesc
; APPLICANT: PIULATS, Jaume
; APPLICANT: ROSELL, Elisabet
; APPLICANT: ADAN, Jaume
; APPLICANT: GOODMAN, Simon
; APPLICANT: HAHN, Diane
; TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,699A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94120165.9
; FILING DATE: 20-DEC-1994

; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1743
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-699A-2

Query Match 91.7%; Score 606; DB 2; Length 127;
Best Local Similarity 90.5%; Pred. No. 1.9e-55;
Matches 114; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVSSAQLGLLLLCFQGTCTCDIQMTQTSSLSASLGRVITISCRASODISSYLNWYQOKP 60
Db 1 MVSSAQLGLLLLCFQGTCTCDIQMTQTSSLSASLGRVITISCRASODISSYLNWYQOKP 60

Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTVKLLIYTSRLHSGVPSRFGSGGCTDYSLTINNLEQEDIATYFCQOGNTLPYTFGG 120

Qy 121 GTKLEI 126
Db 121 GTKVEM 126

RESULT 10
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 8437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10

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Best Local Similarity 86.5%; Pred. No. 3.9e-52;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MMSSAQLGLLLLCFQGTCTCDIQMTQTASSLPASLGRVITISCRASODISSYLNWYQOKP 60
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match      86.8%; Score 574; DB 4; Length 128;
Best Local Similarity 86.5%; Pred. No. 3.9e-52;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MMSAQLGLLLLCFQGTCDIQMTQTASSLPASLGDRVTISCRASQDISYLNWYQKP 60
Qy 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 14
US-08-836-561-29
; Sequence 29, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-561-29

Query Match      84.1%; Score 556; DB 3; Length 127;
Best Local Similarity 84.1%; Pred. No. 2.8e-50;
Matches 106; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

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Qy 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Db 61 DGTIKLIYVTSRLHSGVPSRFGSGGSDYSLTINNLEOEDIATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
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RESULT 15
US-09-434-122-29
; Sequence 29, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6538111uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-NOV-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
; US-09-434-122-29

Query Match      84.1%; Score 556; DB 4; Length 127;
Best Local Similarity 84.1%; Pred. No. 2.8e-50;
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Db 1 MMSSAQFLGILLCFQGTCDIQMTQTSSLSASLGDRVTICGCTSEDIINYNWYRKKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGGTDYSLTINNLEQEDIATYFCQOQNTLPYTFGG 120
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Db 121 GTKLEI 126
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Search completed: October 22, 2003, 22:20:49
Job time : 14.4697 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 22:16:46 ; Search time 23.572 Seconds
(without alignments)
902.237 Million cell updates/sec

Title: US-09-114-285A-29

Perfect score: 661

Sequence: 1 MVSSAFLGLLLLCFQSTRC.....CQGNLPTVFGGTKLEIN 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	96.5	131	8	US-08-779-784-21
2	638	96.5	131	12	US-10-010-729-64
3	626	94.7	127	12	US-10-268-883-5
4	621	93.9	127	15	US-10-084-139-2
5	574	86.8	128	9	US-09-764-304-10
6	574	86.8	128	9	US-09-764-304-19
7	574	86.8	128	12	US-10-166-626-10
8	574	86.8	128	12	US-10-166-626-19
9	574	86.8	128	15	US-10-265-713-10
10	574	86.8	128	15	US-10-265-713-19
11	556	84.1	127	15	US-10-283-349-29
12	534	80.8	108	14	US-10-140-555-4
13	526	79.6	107	12	US-10-268-883-6
14	526	79.6	107	15	US-10-269-010-2
15	524	79.3	601	10	US-09-480-236-1

16	523	79.1	107	12	US-10-310-674A-34	Sequence 34, Appl
17	517	78.2	108	15	US-10-141-908-7	Sequence 7, Appl
18	512	77.5	214	9	US-09-754-998-1	Sequence 1, Appl
19	512	77.5	274	9	US-09-813-659-30	Sequence 30, Appl
20	512	77.5	302	9	US-09-813-659-18	Sequence 18, Appl
21	512	77.5	302	9	US-09-813-659-32	Sequence 32, Appl
22	512	77.5	504	15	US-10-207-655-348	Sequence 348, App
23	508	76.9	127	15	US-10-283-349-71	Sequence 71, Appl
24	506	76.6	127	15	US-10-283-349-103	Sequence 103, App
25	505	76.4	107	15	US-10-011-931-4	Sequence 4, Appl
26	496	75.0	127	15	US-10-283-349-98	Sequence 98, Appl
27	493	74.6	127	15	US-10-283-349-88	Sequence 88, Appl
28	492	74.4	127	15	US-10-283-349-92	Sequence 92, Appl
29	487	73.7	108	9	US-09-056-160B-10	Sequence 10, Appl
30	487	73.7	108	12	US-10-234-671-10	Sequence 10, Appl
31	486	73.5	109	15	US-10-197-080-4	Sequence 4, Appl
32	478	72.3	109	11	US-09-929-665-21	Sequence 21, Appl
33	478	72.3	109	11	US-09-929-546-21	Sequence 21, Appl
34	463	70.0	127	15	US-10-084-139-6	Sequence 6, Appl
35	459	69.4	107	11	US-09-892-613C-10	Sequence 10, Appl
36	456	69.0	108	9	US-09-905-243-73	Sequence 73, Appl
37	456	69.0	130	8	US-08-779-784-35	Sequence 35, Appl
38	456	69.0	130	12	US-10-010-729-71	Sequence 71, Appl
39	449	67.9	234	9	US-09-740-002-24	Sequence 24, Appl
40	447	67.6	105	15	US-10-141-908-31	Sequence 31, Appl
41	447	67.6	214	9	US-09-940-166A-2	Sequence 2, Appl
42	447	67.6	214	9	US-09-811-384-11	Sequence 11, Appl
43	447	67.6	236	10	US-09-859-053-30	Sequence 30, Appl
44	447	67.6	237	9	US-09-940-166A-6	Sequence 6, Appl
45	447	67.6	237	15	US-10-227-694-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-779-784-21
; Sequence 21, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA

RESULT 6
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA

```

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
; US-09-764-304-19

Query Match      86.8%; Score 574; DB 9; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy      1  MVSSAQFLGLLLCFQGTCDIQMTTSSLASGLDRVTISCRASODISSYLNWYQOKP 60
Db      1  MMSSAQFLGLLLCFQGTCDIQMTAGSSLPASLGLDRVTISCSASODISNLYNWOQKP 60

Qy      61  DGTIKLLIYYTSELHSGVPSRSGSGCTDYSLTNNLQEDIDATVFCQOGNTLPYTFGG 120
Db      61  DGTVKLLIFYSNHLHSGVPSRFGSGSGTDYSLTNNLEPDIDATVFCQYKSLPWTTFGG 120

Qy      121  GTKLEI 126
Db      121  GTKLEI 126

RESULT 7
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10

```

```
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match      86.8%; Score 574; DB 12; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MWSSAQFLGLLLCFQGTCDIQMTTASSLPASLGDRVTISCSASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 61 DGTIKLLIYVTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQGNLTLPYTFGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 DGTVKKLLIFSYSNLHSGVPSRFGSGGSDTYSLTISNLEPEDATYFCHQYKLPWTFTGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 8
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR FILING DATE: 1995-05-31
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1994-08-17
; PRIOR FILING DATE: 1992-09-17
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19

Query Match      86.8%; Score 574; DB 12; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MWSSAQFLGLLLCFQGTCDIQMTTASSLPASLGDRVTISCSASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 61 DGTIKLLIYVTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQGNLTLPYTFGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 DGTVKKLLIFSYSNLHSGVPSRFGSGGSDTYSLTISNLEPEDATYFCHQYKLPWTFTGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
QY 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 9
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match      86.8%; Score 574; DB 15; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVSSAQFLGLLLCFQGTCDIQMTTSSLSASLGDRVTISCRASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MWSSAQFLGLLLCFQGTCDIQMTTASSLPASLGDRVTISCSASQDISYLNWYQKP 60
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 61 DGTIKLLIYVTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQGNLTLPYTFGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 DGTVKKLLIFSYSNLHSGVPSRFGSGGSDTYSLTISNLEPEDATYFCHQYKLPWTFTGG 120
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 GTKLEI 126
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 10
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
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; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-265-713-19

Query Match 86.8%; Score 574; DB 15; Length 128;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MVSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 11
US-10-283-349-29
; Sequence 29, Application US/10283349
; Publication No. US20030096977A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, No. US20030096977A1uo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-283-349-29

Query Match 84.1%; Score 556; DB 15; Length 127;
Best Local Similarity 84.1%; Pred. No. 5.3e-44;
Matches 106; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MVSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Db 1 MMSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKP 60
Qy 61 DGTIKLLIYTSRLHSGVPSRFGSGGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGG 120
Db 61 DGTVELLIYTSRLQSGVPSRFGSGGSDTYSLTISDLEQEDATYFCQOGNTLPYTVGG 120
Qy 121 GTKLEI 126
Db 121 GTKLEI 126

RESULT 12
US-10-140-555-4
; Sequence 4, Application US/10140555
; Publication No. US20020127227A1
; GENERAL INFORMATION:
; APPLICANT: Julie A. Abrahamson
; APPLICANT: Stephen D. Holmes
; APPLICANT: Jeffrey R. Jackson
; TITLE OF INVENTION: RHAMM Antagonist Antibodies
; FILE REFERENCE: PS0857
; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-140-555-4

Query Match 80.8%; Score 534; DB 14; Length 108;
Best Local Similarity 96.2%; Pred. No. 4.7e-42;
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKPDGTLKLIYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQOKPDGTLKLIYTSRLHSGVPS 60
Qy 81 RFGSGGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 126
Db 61 RFGSGGSDTYSLTINNLEQEDATYFCQOGNTLPYTFGGGTKLEI 106

RESULT 13
US-10-268-883-6
; Sequence 6, Application US/10268883
; Publication No. US2003013862A1
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Green, Jennifer Macphate
; TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
; FILE REFERENCE: 05882.0062.NPUS01
; CURRENT APPLICATION NUMBER: US/10/268,883
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: USSN 60/329,178
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: USSN 60/331,965
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mouse
US-10-268-883-6

Query Match 79.6%; Score 526; DB 12; Length 107;
Best Local Similarity 93.4%; Pred. No. 2.6e-41;
Matches 99; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRSSQDISKYLNNWYQKPDGTIKLLIYYTSRLHSGVPS 60
Qy 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEI 126
Db 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGGDTPVTFGGGKLEI 106

RESULT 14
US-10-269-010-2
; Sequence 2, Application US/10269010
; Publication No. US20030096285A1
; GENERAL INFORMATION:
; APPLICANT: Tso, J.
; APPLICANT: Tso, Jennifer
; TITLE OF INVENTION: ANTI-HLA-DR ANTIBODIES AND THE METHODS OF USE THEREOF
; FILE REFERENCE: 05882.0062.NPUS01
; CURRENT APPLICATION NUMBER: US/10/269,010
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: USSN 60/329,178
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: USSN 60/331,965
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mouse
US-10-269-010-2

Query Match 79.6%; Score 526; DB 15; Length 107;
Best Local Similarity 93.4%; Pred. No. 2.6e-41;
Matches 99; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYTSRLHSGVPS 80
Db 1 DIQMTQTSSLSASLGDRVTISCRSSQDISKYLNNWYQKPDGTIKLLIYYTSRLHSGVPS 60
Qy 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEI 126
Db 61 RFGSGSGTDYSLTINNLEQEDIATYFCQGGDTPVTFGGGKLEI 106

RESULT 15
US-09-480-236-1
; Sequence 1, Application US/09480236
; Patent No. US20020142000A1
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480,236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: scFv(UCHT-1)-PE38 amino acid sequence
US-09-480-236-1

Query Match 79.3%; Score 524; DB 10; Length 601;
Best Local Similarity 93.4%; Pred. No. 2.7e-40;
Matches 99; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYTSRLHSGVPS 80
Db 3 DIQMTQTSSLSASLGDRVTISCRASQDIRNLYNQKPDGTIKLLIYYTSRLHSGVPS 62
Qy 81 RFGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEI 126
Db 63 RFGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPWTFAGGKLEI 108

Search completed: October 22, 2003, 22:21:45
Job time : 24.572 secs